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OM protein - protein search, using sw model

Run on: September 23, 2004, 21:02:22 ; Search time 96 Seconds
(without alignments)
950.655 Million cell updates

Title: US-09-397-342C-1

Perfect score:

Sequence: 1 MSVPEEEERLLPLTQRWPR.....SMVFWLTYEKIREMSGVSPF 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : A_Geneseq_29Jan04:
1: Genesexp1950s:*
2: Genesexp1950s:*
3: Genesexp2000s:*
4: Genesexp2001s:*
5: Genesexp2002s:*
6: Genesexp2003s:*
7: Genesexp2003bs:*
8: Genesexp2004s:*
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SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1690	100.0	323	3	AAy81497	Aay81497 Human unc
2	1690	100.0	323	3	AAy99457	Aay99457 Human unc
3	1690	100.0	323	4	AAy66206	Aay66206 Protein o
4	1690	100.0	323	4	AAb87588	Aab87588 Human PRO
5	1690	100.0	323	5	ABg95913	Abg95913 Human sec
6	1690	100.0	323	6	ABu90938	Abu90938 Novel hum
7	1690	100.0	323	6	ABo33997	AbO33997 Human sec
8	1690	100.0	323	6	ABu72014	Abu72014 Novel hum
9	1690	100.0	323	6	ABu71568	Abu71568 Human sec
10	1690	100.0	323	6	ABU72349	AbU72349 Human PRO
11	1690	100.0	323	6	ABu91022	Abu91022 Human PRO
12	1690	100.0	323	6	ABo27343	AbO27343 Human sec
13	1690	100.0	323	6	ABU92538	AbU92538 Human sec
14	1690	100.0	323	6	ABu81208	Abu81208 Human sec
15	1690	100.0	323	6	ABO53322	AbO53322 Novel hum
16	1690	100.0	323	6	ABu98325	Abu98325 Novel hum
17	1690	100.0	323	6	ABu89330	Abu89330 Novel hum
18	1690	100.0	323	6	ABu82537	Abu82537 Novel hum
19	1690	100.0	323	6	ABU96501	AbU96501 Human PRO
20	1690	100.0	323	6	ABu72171	Abu72171 Human PRO
21	1690	100.0	323	6	ADb17183	Adb17183 Human tra
22	1690	100.0	323	6	ABo44301	AbO44301 Human sec
23	1690	100.0	323	6	ABO33699	AbO33699 Novel hum
24	1690	100.0	323	6	ADa19988	Ada19988 Novel hum
25	1690	100.0	323	6	ADb17371	Adb17371 Human tra

ALIGNMENTS

RESULT 1

RESOL 1
AAY81497
ID AAY81497 standard; protein; 323 AA.

AC AAY81497;

DT 21-JUL-2000 (first entry)

Human uncoupling protein UCP4.

Uncoupling protein; UCP4; expressed sequence tag; EST; human; KW

chromosome 6p11.2-q12; ATP synthesis; energy efficiency;

mitochondrial membrane; proton leakage; heat production; metabolic rate; drug screening; obesity; sepsis; stroke; trauma; sepsis; infection.

OS Homo sapiens.

Key	Location/Qualifiers
FT Domain	22..41
FT Domain	/note= "Transmembrane domain I"
FT Region	39..47
FT Region	/note= "Putative mitochondrial carrier protein motif"
FT Domain	88..109
FT Domain	/note= "Transmembrane domain II"
FT Domain	128..145
FT Domain	/note= "Transmembrane domain III"
FT Region	147..153
FT Region	/note= "Putative mitochondrial carrier protein motif"
FT Domain	195..212
FT Domain	/note= "Transmembrane domain IV"
FT Domain	229..248
FT Domain	/note= "Transmembrane domain V"
FT Region	248..253
FT Region	/note= "Putative mitochondrial carrier protein motif"
FT Binding-site	284..293
FT Binding-site	/note= "Nucleotide binding domain"
FT Domain	288..311
FT Domain	/note= "Transmembrane domain VI"
XX	
PN WO200017353-A1.	
XX	
XX 30-MAR-2000.	
XX	
XX 15-SEP-1999;	99WO-US021194.
XX	
PR 22-SEP-1998;	98US-0101279P.
PR 30-DEC-1998;	98US-0114223P.
PR 16-APR-1999;	99US-0129674P.

XX (GETH) GENENTECH INC.
 PA Adams S, Pan J, Zhong A;
 XX WPI; 2000-292842/25.
 XX N-PSDB; AAA14084.
 XX New nucleic acid encoding human uncoupled protein-4, useful e.g for
 PT identifying metabolic regulators for treatment of obesity.
 XX Claim 1; Fig 1; 80pp; English.
 XX This sequence represents human uncoupling protein UCP4. The human UCP4
 CC cDNA (ATCC 203124) was isolated from a brain cDNA library using a probe
 CC generated using primers AAA14086-A14087. These primers were based on a
 CC UCP4 "from DNA" sequence (AAA14085) derived from a number of ESTs
 CC (expressed sequence tags) which were selected on the basis of homology
 CC with human UCP3. The human UCP4 gene has been mapped to chromosome 6p11.2
 CC -q12. UCP4 catalyzes the leakage of protons through the mitochondrial
 CC membrane, thus bypassing ATP synthase and thereby reducing the efficiency
 CC of ATP synthesis. Modulation of UCP4 activity or expression can therefore
 CC alter the metabolic rate and heat production via modulation of ATP
 CC synthetic efficiency. UCP4 nucleic acids may be used for recombinant
 CC production of UCP4 and as a source of primers and hybridisation probes
 CC which may be used for the analysis of UCP4 expression, for screening for
 CC homologous sequences, and for chromosome or gene mapping. They can be
 CC also be used to produce transgenic or knockout animals for the
 CC development and screening of therapeutic agents, as a source of antisense
 CC nucleotides, and in gene therapy for metabolic disorders. The UCP4
 CC protein can be used to screen for specific modulators of activity and to
 CC raise antibodies which may be used therapeutically as UCP4 antagonists or
 CC UCP4 targeting proteins, for affinity purification of UCP4, and as
 CC immunosay reagents for detecting UCP4 expression, e.g., for the
 CC diagnosis of impaired neural activity or neural degeneration. Agents that
 CC modulate UCP4 activity are used to control the metabolic rate in mammals.
 CC UCP4 upregulators can be used to increase the metabolic rate in order to
 CC treat obesity and the symptoms associated with stroke, trauma, sepsis and
 CC infection
 XX
 SQ Sequence 323 AA;
 Query Match 100.0%; Score 1690; DB 3; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPEEERLLPTQWRPRASKFLLSGCAATVAELATFPDLTKTRIQMGGEAALARLGD 60
 Db 1 MSVPEEERLLPTQWRPRASKFLLSGCAATVAELATFPDLTKTRIQMGGEAALARLGD 60
 QY 61 GABESAPYRCMVRTALGIIIEEGFLKLQGVTPAIYRHVVYSGRMVYVYHLREVVFGKS 120
 Db 61 GABESAPYRCMVRTALGIIIEEGFLKLQGVTPAIYRHVVYSGRMVYVYHLREVVFGKS 120
 QY 121 EDEHYPLKWSVIGMWAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRGRVHHAFKI 180
 Db 121 EDEHYPLKWSVIGMWAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRGRVHHAFKI 180
 QY 181 LAEGGIRGLWAGVNPINQRAALVNMGLTYYTDYTKHYLVNLTPELDNIMTHGLSSLCGSL 240
 Db 181 LAEGGIRGLWAGVNPINQRAALVNMGLTYYTDYTKHYLVNLTPELDNIMTHGLSSLCGSL 240
 QY 241 VASILGTPADVIKSRINQPRDKQGRGLLYKSTDCGLIQAVQEGFMSLYKGLPSPWLRM 300
 Db 241 VASILGTPADVIKSRINQPRDKQGRGLLYKSTDCGLIQAVQEGFMSLYKGLPSPWLRM 300
 QY 301 TPMSVMFWLTYEKIRENSGVSPF 323
 Db 301 TPMSVMFWLTYEKIRENSGVSPF 323
 RESULT 2
 AAY99457

ID XX
 AC AAY99457;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Human UCP4 amino acid sequence SEQ ID NO:406.
 XX
 KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
 XX
 OS Homo sapiens.
 XX
 PN WO200012708-A2.
 XX
 PD 09-MAR-2000.
 XX
 PF 01-SEP-1999; 99WO-US020111.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 01-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0098536P.
 PR 09-SEP-1998; 98US-0098596P.
 PR 09-SEP-1998; 98US-0098598P.
 PR 09-SEP-1998; 98US-0098602P.
 PR 09-SEP-1998; 98US-0098642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.

PR	29-SEP-1998;	98US-0102330P.	DR	WPI; 2000-237871/20.
PR	29-SEP-1998;	98US-0102331P.	XX	N-PSDB; AAA37139.
PR	30-SEP-1998;	98US-0102484P.	XX	
PR	30-SEP-1998;	98US-0102487P.	PT	New mammalian DNA sequences encoding transmembrane, receptor or secreted
PR	30-SEP-1998;	98US-0102570P.	PT	PRO polypeptides, useful for screening of potential peptide or small
PR	30-SEP-1998;	98US-0102571P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.
PR	01-OCT-1998;	98US-0102684P.	XX	
PR	01-OCT-1998;	98US-0102687P.	PS	Claim 12; Fig 236; 773pp; English.
PR	02-OCT-1998;	98US-0102965P.	XX	
PR	06-OCT-1998;	98US-0103258P.	CC	AAA37022 to AAA37144 encode the new isolated human transmembrane,
PR	07-OCT-1998;	98US-0103449P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
PR	07-OCT-1998;	98US-0103314P.	CC	transmembrane and receptor PRO proteins can be used for screening of
PR	07-OCT-1998;	98US-0103315P.	CC	potential peptide or small molecule inhibitors of the relevant
PR	07-OCT-1998;	98US-0103328P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences
PR	07-OCT-1998;	98US-0103395P.	CC	encoding then have various industrial applications, including uses as
PR	07-OCT-1998;	98US-0103396P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
PR	07-OCT-1998;	98US-0103401P.	CC	primers and hybridisation probes used in the isolation of the PRO
PR	08-OCT-1998;	98US-0103633P.	CC	polypeptides from the present invention
PR	08-OCT-1998;	98US-0103678P.	XX	
PR	08-OCT-1998;	98US-0103679P.	SQ	Sequence 323 AA;
PR	14-OCT-1998;	98US-0103711P.		
PR	14-OCT-1998;	98US-0104257P.		
PR	20-OCT-1998;	98US-0104987P.		
PR	20-OCT-1998;	98US-0105000P.		
PR	20-OCT-1998;	98US-0105104P.		
PR	22-OCT-1998;	98US-0105169P.		
PR	22-OCT-1998;	98US-0105266P.		
PR	26-OCT-1998;	98US-0105693P.		
PR	26-OCT-1998;	98US-0105694P.		
PR	27-OCT-1998;	98US-0105807P.		
PR	27-OCT-1998;	98US-0105881P.		
PR	27-OCT-1998;	98US-0105882P.		
PR	27-OCT-1998;	98US-0106062P.		
PR	28-OCT-1998;	98US-0106023P.		
PR	28-OCT-1998;	98US-0106029P.		
PR	28-OCT-1998;	98US-0106030P.		
PR	28-OCT-1998;	98US-0106032P.		
PR	28-OCT-1998;	98US-0106033P.		
PR	28-OCT-1998;	98US-0106178P.		
PR	29-OCT-1998;	98US-0106248P.		
PR	29-OCT-1998;	98US-0106384P.		
PR	29-OCT-1998;	98US-0108500P.		
PR	30-OCT-1998;	98US-0106464P.		
PR	03-NOV-1998;	98US-0106856P.		
PR	03-NOV-1998;	98US-0106902P.		
PR	03-NOV-1998;	98US-0106905P.		
PR	03-NOV-1998;	98US-0106919P.		
PR	03-NOV-1998;	98US-0106932P.		
PR	03-NOV-1998;	98US-0106934P.		
PR	10-NOV-1998;	98US-0107783P.		
PR	17-NOV-1998;	98US-0108775P.		
PR	17-NOV-1998;	98US-0108779P.		
PR	17-NOV-1998;	98US-0108787P.		
PR	17-NOV-1998;	98US-0108788P.		
PR	17-NOV-1998;	98US-0108801P.		
PR	17-NOV-1998;	98US-0108802P.		
PR	17-NOV-1998;	98US-0108806P.		
PR	17-NOV-1998;	98US-0108807P.		
PR	17-NOV-1998;	98US-0108867P.		
PR	17-NOV-1998;	98US-0108925P.		
PR	18-NOV-1998;	98US-0108848P.		
PR	18-NOV-1998;	98US-0108849P.		
PR	18-NOV-1998;	98US-0108850P.		
PR	18-NOV-1998;	98US-0108851P.		
PR	18-NOV-1998;	98US-0108852P.		
PR	18-NOV-1998;	98US-0108858P.		
PR	18-NOV-1998;	98US-0108904P.		
XX				
PA	(GETH) GENENTECH INC.			
XX				
PI	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;			
XX				

PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2001-071395/08.
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX
 PS Claim 1; Fig 236; 787pp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX
 SQ Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 4; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKRLQMGGAALRLGD 60
 DB 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKRLQMGGAALRLGD 60
 QY 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 DB 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 QY 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRFRGVHHAFAKI 180
 DB 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRFRGVHHAFAKI 180
 QY 181 LAEGGIRGLWAGWPNIQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCGL 240
 DB 181 LAEGGIRGLWAGWPNIQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCGL 240
 QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGLFPSWLRM 300
 DB 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGLFPSWLRM 300
 QY 301 TPMSVFWLTYEKIREMSGVSPP 323
 DB 301 TPMSVFWLTYEKIREMSGVSPP 323

RESULT 4
 AAB87588
 ID AAB87588 standard; protein; 323 AA.
 XX
 AC AAB87588;
 XX
 XX 15-MAY-2001 (first entry)
 DT
 XX Human PRO1566.
 DE
 XX Human; PRO protein; mapping.
 KW

XX OS Homo sapiens.
 XX WO200116318-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-US023328.
 XX
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 PI
 XX WPI; 2001-183260/18.
 DR N-PSDB; AAF92120.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX
 PS Claim 12; Fig 126; 278pp; English.
 XX
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein.
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridisation probes, and in chromosome and gene mapping
 XX
 SQ Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 4; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKRLQMGGAALRLGD 60
 DB 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKRLQMGGAALRLGD 60
 QY 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 DB 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 QY 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRFRGVHHAFAKI 180
 DB 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRFRGVHHAFAKI 180
 QY 181 LAEGGIRGLWAGWPNIQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCGL 240
 DB 181 LAEGGIRGLWAGWPNIQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCGL 240
 QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGLFPSWLRM 300
 DB 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGLFPSWLRM 300

QY 301 TPWSMVFWLTYKIREMSGVSPF 323
 |||||
 Db 301 TPWSMVFWLTYKIREMSGVSPF 323

RESULT 5
 ABG95913
 ID ABG95913 standard; protein; 323 AA.
 AC ABG95913;
 XX
 DT 10-DEC-2002 (first entry)
 DE Human secreted/transmembrane protein PRO1566.
 DE
 XX Human; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2002119130-A1.
 XX
 PD 29-AUG-2002.
 XX
 XX 06-DEC-2001; 2001US-00006867.
 XX
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 22-APR-1998; 98US-0082797P.
 PR 29-APR-1998; 98US-0083495P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0097633P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100663P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.

PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 24-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023328.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-731348/79.
 DR N-PSDB; ABS74440.
 XX
 XX New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 PS
 PS Claim 20; Fig 126; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for

identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic antibody reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence represents a novel secreted or transmembrane protein of the invention

XX Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 5; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLMQGEAALARLGD 60
 Db 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLMQGEAALARLGD 60

Qy 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120
 Db 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120

Qy 121 EDEHYPLKWSVIGGMAGVIGQFLANPTDLVKVQMEGRKLEKPLRFRGVHFAFI 180
 Db 121 EDEHYPLKWSVIGGMAGVIGQFLANPTDLVKVQMEGRKLEKPLRFRGVHFAFI 180

Qy 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240
 Db 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240

Qy 241 VASILGTPADVTKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGLPSWLRM 300
 Db 241 VASILGTPADVTKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGLPSWLRM 300

Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
 Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 6
 ABU90938 ID ABU90938 standard; protein; 323 AA.
 AC ABU90938;
 XX 11-JUL-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO1566.
 XX Human; secreted and transmembrane protein; PRO; antibody therapy;
 KW pharmaceutical; diagnostic; biosensor; bioreactor.
 XX Homo sapiens.
 OS US2003018173-A1.
 XX 23-JAN-2003.
 XX 01-MAY-2002; 2002US-00063515.
 XX 06-DEC-2001; 2001US-00006867.
 XX (GETH) GENENTECH INC.
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 WPI; 2003-401702/38.
 DR N-PSDB; ACA91226.

XX New antibody useful for identifying PRO polypeptides, for affinity purification of PRO polypeptides, and for preparing a medicament for diagnosing or treating conditions responsive to the antibody or PRO polypeptide.

XX Disclosure; Fig 126; 345pp; English.

XX The invention describes an antibody that specifically binds to a PRO polypeptide having a fully defined amino acid sequence given in the specification. The antibody is useful in identifying PRO polypeptides useful for various industrial applications, including pharmaceuticals, diagnostics, biosensors and bioreactors. The antibody is also used for affinity purification of PRO polypeptides from recombinant cell culture or natural sources. The antibody, PRO polypeptide, or its agonists or antagonists, may be used for preparing a medicament for diagnosing or treating a condition responsive to the antibody, PRO polypeptide, or its agonists or antagonists. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

XX Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLMQGEAALARLGD 60
 Db 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLMQGEAALARLGD 60

Qy 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120
 Db 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120

Qy 121 EDEHYPLKWSVIGGMAGVIGQFLANPTDLVKVQMEGRKLEKPLRFRGVHFAFI 180
 Db 121 EDEHYPLKWSVIGGMAGVIGQFLANPTDLVKVQMEGRKLEKPLRFRGVHFAFI 180

Qy 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240
 Db 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240

Qy 241 VASILGTPADVTKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGLPSWLRM 300
 Db 241 VASILGTPADVTKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGLPSWLRM 300

Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
 Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 7
 AB033997 ID AB033997 standard; protein; 323 AA.
 XX AB033997;
 AC AB033997;
 XX 18-SEP-2003 (first entry)
 DE Human secreted/transmembrane protein PRO1566.
 XX Human; secreted/transmembrane protein; PRO; tumour; cancer; cytostatic.
 KW Homo sapiens.
 OS US2003009013-A1.
 XX 09-JAN-2003.
 XX

CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
 CC assays to identify other proteins or molecules involved in binding
 CC reaction, to generate transgenic animals or knockout animals, which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents, for chromosome identification, and tissue typing. The
 CC PRO polypeptides and nucleic acid molecules are also useful in gene
 CC therapy, and as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. This is the amino acid sequence of a novel
 CC human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 323 AA;
 Query Match 100.0%; Score 1690; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPDEERLLPTQWRPRASKFLLSGCAATVAELATFFLDLTKTRLOMQGEAALRLGD 60
 DB 1 MSVPDEERLLPTQWRPRASKFLLSGCAATVAELATFFLDLTKTRLOMQGEAALRLGD 60
 QY 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
 DB 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
 QY 121 EDEHYPLWKSIVGGMAWVIGQFLANPTDLVKVQMMEGKRLGKPLRFRGVHFAFI 180
 DB 121 EDEHYPLWKSIVGGMAWVIGQFLANPTDLVKVQMMEGKRLGKPLRFRGVHFAFI 180
 QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTYYDTVGHVLTNTPLEDNIMTHGLSSLSGL 240
 DB 181 LAEGGIRGLWAGWPNIQRAALVNMGLTYYDTVGHVLTNTPLEDNIMTHGLSSLSGL 240
 QY 241 VASITGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGLFPLSLRM 300
 DB 241 VASITGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGLFPLSLRM 300
 QY 301 TPWSMVFWLTVEKIREMSGVSPF 323
 DB 301 TPWSMVFWLTVEKIREMSGVSPF 323
 RESULT 9
 ABU71568
 ID ABU71568 standard; protein; 323 AA.
 AC ABU71568;
 DT 10-JUN-2003 (first entry)
 XX Human secreted polypeptide PRO1566.
 DE Human; gene therapy; tumour; cancer.
 KW Homo sapiens.
 OS US2003013855-A1.
 FN 16-JAN-2003.
 PD 03-MAY-2002; 2002US-00063616.
 PF 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAY-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 XX (GETH) GENENTECH INC.
 PA Eaton DL, Filvaroff E, Gezritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-330485/31.
 DR N-PSDB; ACA58872.
 XX
 PT New isolated antibody specifically binding a PRO polypeptide, useful for
 PT the preparation of a medicament for treating disorders with the aberrant
 PT expression or activity of the PRO polypeptide, such as tumor conditions
 PT and cancer.
 XX Disclosure; Page 198-199; 406pp; English.
 PS The invention relates to an antibody that binds to a polypeptide with a
 CC fully defined sequence given in the specification. The methods and
 CC compositions (containing antibodies that specifically bind a PRO
 CC polypeptide) of the present invention are useful for the preparation of a
 CC medicament for the treatment of disorders associated with the aberrant
 CC expression or activity of the PRO polypeptide, such as tumour conditions
 CC and cancer. They can also be used to generate transgenic or knockout
 CC animals useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
 CC molecular weight markers for protein electrophoresis, chromosome
 CC identification and tissue typing. The PRO polypeptides are useful to
 CC induce angiogenesis e.g wound healing; in the treatment of sports-related
 CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
 CC antibodies may be used in various diagnostic, competitive binding and/or
 CC immunoprecipitation assays. The present sequence represents the amino
 CC acid sequence of a PRO polypeptide of the invention
 XX
 SQ Sequence 323 AA;
 Query Match 100.0%; Score 1690; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPDEERLLPTQWRPRASKFLLSGCAATVAELATFFLDLTKTRLOMQGEAALRLGD 60
 DB 1 MSVPDEERLLPTQWRPRASKFLLSGCAATVAELATFFLDLTKTRLOMQGEAALRLGD 60
 QY 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
 DB 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
 QY 121 EDEHYPLWKSIVGGMAWVIGQFLANPTDLVKVQMMEGKRLGKPLRFRGVHFAFI 180
 DB 121 EDEHYPLWKSIVGGMAWVIGQFLANPTDLVKVQMMEGKRLGKPLRFRGVHFAFI 180
 QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTYYDTVGHVLTNTPLEDNIMTHGLSSLSGL 240
 DB 181 LAEGGIRGLWAGWPNIQRAALVNMGLTYYDTVGHVLTNTPLEDNIMTHGLSSLSGL 240
 QY 241 VASITGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGLFPLSLRM 300
 DB 241 VASITGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGLFPLSLRM 300
 QY 301 TPWSMVFWLTVEKIREMSGVSPF 323
 DB 301 TPWSMVFWLTVEKIREMSGVSPF 323

Db 61 GAREAPYRGWRTALGIIIEEGFLKLWQGVTPAIYRHVYVSGRMVYEHLEWVFGKS 120
Qy 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGGKPLRFRGVHAFPAKI 180
Db 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGGKPLRFRGVHAFPAKI 180
Qy 181 LAEGGIRGLWAGWVNPQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Db 181 LAEGGIRGLWAGWVNPQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Qy 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGFPLPSWLRM 300
Db 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGFPLPSWLRM 300
Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 10
ABU72349
ID ABU72349 standard; protein; 323 AA.
XX AC ABU72349;
XX DT 16-JUN-2003 (first entry)
XX DE Human PRO polypeptide #63.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX KW anti-PRO antibody; diagnostic assay; gene expression.
XX OS Homo sapiens.
XX PN US2002182638-A1.
XX PD 05-DEC-2002.
XX PF 02-MAY-2002; 2002US-00063547.
XX PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 25-AUG-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 23-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
PA (GETH) GENENTECH INC.
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX N-PSDB; ACA64048.
DR WPI; 2003-328612/04.
DR N-PSDB; ACA64048.
XX An isolated secreted transmembrane polypeptide designated PRO, useful as
PT a therapeutic agent.
XX Disclosure; Fig 126; 236pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of a condition responsive to anti-PRO antibody.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
CC its expression in specific cells, tissues or serum, and for affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC ABU72287-ABU72370 represent the human PRO polypeptides of the invention
XX
XX Sequence 323 AA;
Qy 1 MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
Db 1 MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
Qy 61 GAREAPYRGWRTALGIIIEEGFLKLWQGVTPAIYRHVYVSGRMVYEHLEWVFGKS 120
Db 61 GAREAPYRGWRTALGIIIEEGFLKLWQGVTPAIYRHVYVSGRMVYEHLEWVFGKS 120
Qy 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGGKPLRFRGVHAFPAKI 180
Db 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGGKPLRFRGVHAFPAKI 180
Qy 181 LAEGGIRGLWAGWVNPQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Db 181 LAEGGIRGLWAGWVNPQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Qy 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGFPLPSWLRM 300
Db 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGFPLPSWLRM 300
Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 11
ABU91022
ID ABU91022 standard; protein; 323 AA.
XX AC ABU91022;
XX DT 14-JUL-2003 (first entry)
XX DE Human PRO polypeptide #63.
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;
KW lung; stomach; oesophageal; skin; tumour; cancer; cytostatic.
XX OS Homo sapiens.

XX US2003018168-A1.
 PN XX
 XX 23-JAN-2003.
 PD
 XX 02-MAY-2002; 2002US-00063569.
 XX
 PR 30-DEC-1998; 98XR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 22-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 10-NOV-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-0074259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 08-DEC-2001; 2001US-00006867.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 PI
 XX WPI; 2003-401699/38.
 DR N-PSDB; ACA91312.
 DR
 XX New isolated, secreted and transmembrane PRO polypeptide, useful for the
 PT diagnosis, prevention and treatment of rectal, lung, stomach, esophageal
 PT or skin cancers.
 XX
 XX Disclosure; Fig 126; 235pp; English.
 PS
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO polypeptide
 CC and polynucleotide sequences are useful for the diagnosis, prevention and
 CC treatment of rectal, lung, stomach, oesophageal or skin tumours, and/or
 CC cancers. The PRO polypeptides are also useful as molecular weight
 CC markers. The PRO polynucleotide sequences are useful for chromosome
 CC identification, hybridisation probes, and for screening libraries of
 CC human cDNA, genomic DNA or mRNA. They may also be used in gene therapy,
 CC particularly for replacing a defective gene. ABU90960-ABU91043 represent
 CC the human PRO polypeptides of the invention
 XX
 SQ Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPPEERLLPLTORWPRASKFLLSGCAATVAELATPDLTKTRLQMOGEAALARLGD 60
 DB 1 MSVPPEERLLPLTORWPRASKFLLSGCAATVAELATPDLTKTRLQMOGEAALARLGD 60
 QY 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPALYRHVVYSGRMVTVYEHLEVVVFGKS 120
 DB 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPALYRHVVYSGRMVTVYEHLEVVVFGKS 120
 QY 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMQMEGRKLEKPLFRGVHAFAXI 180
 DB 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMQMEGRKLEKPLFRGVHAFAXI 180
 QY 181 LAEGGIRGLWAGWPNIQRAALVNMGDLTYYTVKHVLTNPLEDNIMTHGLSSLCSSL 240
 DB 181 LAEGGIRGLWAGWPNIQRAALVNMGDLTYYTVKHVLTNPLEDNIMTHGLSSLCSSL 240
 QY 241 VASIIIGTPADVIKSRIMNQPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGFPLPSWLRM 300
 DB 241 VASIIIGTPADVIKSRIMNQPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGFPLPSWLRM 300
 QY 301 TPWSMVFWLTIEKIREMSGVSPF 323
 DB 301 TPWSMVFWLTIEKIREMSGVSPF 323
 RESULT 12
 ABO27343
 ID ABO27343 standard; protein; 323 AA.
 AC ABO27343;
 XX
 DT 11-SEP-2003 (first entry)
 DE Human secreted/transmembrane polypeptide PRO1566.
 XX Human; tumour; cancer; gene therapy; tissue typing.
 OS Homo sapiens.
 XX
 PN US2003009012-A1.
 XX
 PD 09-JAN-2003.
 XX
 XX 01-MAY-2002; 2002US-00063517.
 XX
 PR 30-DEC-1998; 98XR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 01-FEB-2000; 2000WO-US004341.
 PR 18-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 22-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 10-NOV-2000; 2000WO-US032678.

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PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 30-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-447383/42.
XX N-PSDB; ACD45211.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful for
XX the preparation of a medicament for treating disorders with the aberrant
XX expression or activity of the PRO polypeptide, such as tumor conditions
XX and cancer.
XX
XX Disclosure; Fig 126; 223pp; English.
XX
XX The invention relates to an antibody that binds to a secreted and
XX transmembrane PRO polypeptide. The methods and compositions of the
XX present invention are useful for the preparation of a medicament for the
XX treatment of disorders associated with the aberrant expression or
XX activity of the PRO polypeptide, such as tumor conditions and cancer.
XX They can also be used to generate transgenic or knockout animals useful
XX in the development and screening of therapeutically useful reagents. The
XX PRO polypeptides and encoding nucleic acids can be used as molecular
XX weight markers for protein electrophoresis, chromosome identification and
XX tissue typing. The antibodies may be used in various diagnostic,
XX competitive binding and/or immunoprecipitation assays. The present
XX sequence represents the amino acid sequence of a secreted and
XX transmembrane PRO polypeptide
XX
XX SQ Sequence 323 AA;
XX
XX Query Match 100.0%; Score 1690; DB 6; Length 323;
XX Best Local Similarity 100.0%; Pred. No. 2e-165;
XX Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSVPEEERLLPTQWRPRASKFLSGCAATVAELATFFLDLTKTRLQMGEEAALRLGD 60
XX DB 1 MSVPEEERLLPTQWRPRASKFLSGCAATVAELATFFLDLTKTRLQMGEEAALRLGD 60
XX
XX QY 61 GAREAPYRGWRTALGIIEEGFLKMQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
XX DB 61 GAREAPYRGWRTALGIIEEGFLKMQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
XX
XX QY 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMGEGRKLEKPLRFRGVHFAFAKI 180
XX DB 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMGEGRKLEKPLRFRGVHFAFAKI 180
XX
XX QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTITDYTKVHLVNTPLEDINTHGLSSLCISGL 240
XX DB 181 LAEGGIRGLWAGWPNIQRAALVNMGLTITDYTKVHLVNTPLEDINTHGLSSLCISGL 240
XX
XX QY 241 VASILGTADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFGMSLYKGLFPLSLRM 300
XX DB 241 VASILGTADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFGMSLYKGLFPLSLRM 300
XX
XX QY 301 TPWSMVFWLTYEKIREMSGVSPF 323
XX DB 301 TPWSMVFWLTYEKIREMSGVSPF 323
```

```
RESULT 13
ABU92538
ID ABU92538 standard; protein; 323 AA.
XX
XX AC ABU92538;
XX
XX DT 17-JUL-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO1566.
XX
XX KW Human; PRO; secreted protein; transmembrane protein; cytostatic;
XX KW vulvular; osteopathic; antiarthritic; antirheumatic; lung tumour;
XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
XX KW liver tumour; tumour necrosis factor; pericyte cell proliferation;
XX KW TNF-alpha; proteoglycans release; cartilage; cancer; wound healing;
XX KW cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
XX OS Homo sapiens.
XX
XX PN US2003045684-A1.
XX
XX PD 06-MAR-2003.
XX
XX PF 02-MAY-2002; 2002US-00063553.
XX
XX PR 30-DEC-1998; 98KR-00062142.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 14-MAY-1999; 99US-00311832.
XX PR 14-MAY-1999; 99WO-US010733.
XX PR 25-AUG-1999; 99US-00380137.
XX PR 25-AUG-1999; 99US-00380138.
XX PR 25-AUG-1999; 99US-00380139.
XX PR 25-AUG-1999; 99US-00380142.
XX PR 15-SEP-1999; 99US-00397342.
XX PR 18-OCT-1999; 99US-00403297.
XX PR 12-NOV-1999; 99US-00423844.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 21-MAR-2000; 2000WO-US007532.
XX PR 02-MAY-2000; 2000WO-US014042.
XX PR 02-JUN-2000; 2000WO-US015264.
XX PR 22-AUG-2000; 2000US-00644848.
XX PR 24-AUG-2000; 2000WO-US023328.
XX PR 18-SEP-2000; 2000US-00664610.
XX PR 18-SEP-2000; 2000US-00665350.
XX PR 08-NOV-2000; 2000US-00709238.
XX PR 01-DEC-2000; 2000WO-US032678.
XX PR 20-DEC-2000; 2000US-00747259.
XX PR 20-DEC-2000; 2000WO-US034956.
XX PR 28-FEB-2001; 2001WO-US006520.
XX PR 22-MAR-2001; 2001US-00816744.
XX PR 10-MAY-2001; 2001US-00854208.
XX PR 30-MAY-2001; 2001US-00854280.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 05-JUN-2001; 2001US-00874503.
XX PR 29-JUN-2001; 2001US-00869599.
XX PR 18-JUL-2001; 2001US-00908827.
XX PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH ) GENENTECH INC.
XX
XX PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-392892/37.
XX N-PSDB; ACA93759.
XX
XX New PRO994 polypeptide, useful for detecting tumors, or for stimulating
```

PT Tumor Necrosis Factor alpha, or pericyte proliferation, especially for
PT treating cancer, cartilage defects, osteoarthritis and rheumatoid
PT arthritis in a mammal.
XX Disclosure; Fig 126; 235pp; English.
XX
PS The invention relates to a new isolated PRO994 polypeptide comprises an
CC amino acid sequence appearing as ABU92499, PRO994 lacking its associated
CC signal peptide, the extracellular domain of PRO994, the extracellular
CC domain of PRO994 (lacking its associated signal peptide) or the protein
CC encoded by the full-length coding sequence of the cDNA ATCC 203018. Also
CC included is a chimeric molecule comprising the PRO994 polypeptide fused
CC to a heterologous amino acid sequence. The PRO polypeptide is useful in
CC pharmaceuticals, diagnostics, biosensors or bioreactors. It is
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood, for stimulating the proliferation of pericyte
CC cells, or stimulating the release of proteoglycans from cartilage. The
CC polypeptide may be employed for a variety of therapeutic purposes, e.g.
CC for treating cancer, wound healing, cartilage defects, osteoarthritis,
CC rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83
CC other PRO polypeptides and their encoding cDNAs. The present sequence
CC represents a PRO polypeptide of the invention
XX
XX Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSVPEEERLLPTQRPASKFLLSGCAATVAELATFPLDLTKRLQMGGAALRLGD 60
Db 1 MSVPEEERLLPTQRPASKFLLSGCAATVAELATFPLDLTKRLQMGGAALRLGD 60
Qy 61 GAREAPYRGVMTALGIIEEGFLKMQGVTPTAIVRHVYVSGRMVYEHLEVVFGKS 120
Db 61 GAREAPYRGVMTALGIIEEGFLKMQGVTPTAIVRHVYVSGRMVYEHLEVVFGKS 120
Qy 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMGEGKLEKPLRGRGVHAFKI 180
Db 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMGEGKLEKPLRGRGVHAFKI 180
Qy 181 LAEGIRGLWAGVNPQRAALVNMGLTITVYVHYLVLTNPEDNIMTHGLSSICSLG 240
Db 181 LAEGIRGLWAGVNPQRAALVNMGLTITVYVHYLVLTNPEDNIMTHGLSSICSLG 240
Qy 241 VASILGTPADVKSIRINQPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGLPSWLRM 300
Db 241 VASILGTPADVKSIRINQPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGLPSWLRM 300
Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 14
ABU81208
ID ABU81208 standard; protein; 323 AA.
XX
AC ABU81208;
XX
XX 23-JUN-2003 (first entry)
XX Human secreted polypeptide PRO1566.
XX Human; affinity purification.
XX Homo sapiens.
OS US2003027212-1A1.
PN 06-FEB-2003.
PD

XX 02-MAY-2002; 2002US-00063544.
PF 30-DEC-1998; 98KR-00062142.
XX 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US0031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00742559.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
WPI; 2003-341840/32.
N-PSDB; ACA67333.

New monoclonal antibody that binds to a secreted and transmembrane
polypeptide, useful for detecting and purifying the polypeptide and also
for treating conditions responsive to the antibody.

Disclosure; Fig 126; 235pp; English.

The invention relates to an antibody that binds to a secreted and
transmembrane polypeptide, PRO1136. The antibody is useful for preparing
a medicament useful in the treatment of a condition responsive to anti-
PRO antibody. The antibody is also useful in diagnostic assays for PRO,
by detecting its expression in specific cells, tissues or serum, and for
affinity purification of PRO from recombinant cell culture or natural
sources. The present sequence represents a cDNA encoding a PRO
polypeptide of the invention

Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSVPEEERLLPTQRPASKFLLSGCAATVAELATFPLDLTKRLQMGGAALRLGD 60
Db 1 MSVPEEERLLPTQRPASKFLLSGCAATVAELATFPLDLTKRLQMGGAALRLGD 60

QY 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
PR |||||
Db 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
QY 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAPAKI 180
PR |||||
Db 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAPAKI 180
QY 181 LAEGGIRGLWAGVNPVNIQRAALVNMGDLTYYDTVKHYLVLTPLEDNIMTHGLSSLC SGL 240
PR |||||
Db 181 LAEGGIRGLWAGVNPVNIQRAALVNMGDLTYYDTVKHYLVLTPLEDNIMTHGLSSLC SGL 240
QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLFSPWLRLM 300
PR |||||
Db 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLFSPWLRLM 300
QY 301 TPWSMVFWLTYEKIREMSGVSPF 323
PR |||||
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 15

ABO53322
ID ABO53322 standard; protein; 323 AA.

AC ABO53322;

XX 14-OCT-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1566.

DE Human; secreted and transmembrane protein; PRO.

KW Homo sapiens.

OS US2003027986-A1.

XX 06-FEB-2003.

XX 02-MAY-2002; 2002US-00063549.

XX 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.

PR 15-SEP-1999; 99US-00397342.

PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.

PR 30-DEC-1999; 99WO-US031274.

PR 18-FEB-2000; 2000WO-US004341.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 21-MAR-2000; 2000WO-US007532.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 08-NOV-2000; 2000US-00709238.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00008867.
XX (GETH) GENENTECH INC.
XX Raton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX N-PSDB; ACH66306.
DR WPI; 2003-456358/43.
XX PRO polypeptide, useful for preparing a medicament for treating a
PT condition associated with PRO polypeptide.
PS Disclosure; Fig 126; 222pp; English.
XX The invention describes an isolated polypeptide having at least 80, 85,
CC 90, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or
CC its extracellular domain; (b) a sequence having 46-335 amino acids,
CC lacking its associated signal peptide; or (c) an amino acid sequence
CC encoded by the full-length coding sequence of the cDNA (ATCC accession
CC number 209956). The PRO (secreted and transmembrane) polypeptide is
CC useful for preparing a medicament for treating a condition associated
CC with PRO polypeptide. This is the amino acid sequence of a novel human
CC secreted and transmembrane PRO polypeptide
XX SQ Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 28-165;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKTRLMQGEAALARLGD 60
PR |||||
Db 1 MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKTRLMQGEAALARLGD 60
QY 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
PR |||||
Db 61 GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
QY 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAPAKI 180
PR |||||
Db 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAPAKI 180
QY 181 LAEGGIRGLWAGVNPVNIQRAALVNMGDLTYYDTVKHYLVLTPLEDNIMTHGLSSLC SGL 240
PR |||||
Db 181 LAEGGIRGLWAGVNPVNIQRAALVNMGDLTYYDTVKHYLVLTPLEDNIMTHGLSSLC SGL 240
QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLFSPWLRLM 300
PR |||||
Db 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLFSPWLRLM 300
QY 301 TPWSMVFWLTYEKIREMSGVSPF 323
PR |||||
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

Search completed: September 24, 2004, 03:52:16
Job time: 100 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 03:51:03 ; Search time 51 Seconds
(without alignments)
326.964 Million cell updates/sec

Title: US-09-397-342C-1

Perfect score: 1690

Sequence: 1 MSVPBEEERLLPLTORPRA.....SMVFWLTYKIREMSGVSPF 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/2/iaa/5B COMB.pdp.*

3: /cgn2_6/prodata/2/iaa/6A COMB.pdp.*

4: /cgn2_6/prodata/2/iaa/6B COMB.pdp.*

5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pdp.*

6: /cgn2_6/prodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	33.1	291	US-09-501-558-2	Sequence 2, Appli
2	557.5	33.0	290	US-09-743-847-2	Sequence 2, Appli
3	557.5	33.0	335	US-09-482-273-118	Sequence 118, App
4	476.5	28.2	309	US-10-001-051B-2	Sequence 2, Appli
5	475.5	28.1	312	US-09-142-565-2	Sequence 2, Appli
6	475.5	28.1	312	US-09-808-457-2	Sequence 2, Appli
7	475.5	28.1	312	US-09-423-410-4	Sequence 4, Appli
8	473.5	28.0	309	US-09-743-847-4	Sequence 4, Appli
9	472.5	28.0	299	US-08-518-878B-56	Sequence 56, Appl
10	472.5	28.0	299	US-08-470-868A-56	Sequence 56, Appl
11	472.5	28.0	309	US-08-518-878B-51	Sequence 51, Appl
12	472.5	28.0	309	US-08-807-861A-51	Sequence 51, Appl
13	472.5	28.0	309	US-08-470-868A-51	Sequence 51, Appl
14	472.5	28.0	309	US-08-946-719A-51	Sequence 51, Appl
15	472.5	28.0	309	US-08-946-719A-51	Sequence 51, Appl
16	472.5	28.0	309	US-09-547-983-51	Sequence 51, Appl
17	472.5	28.0	432	US-08-937-466-4	Sequence 4, Appli
18	472.5	28.0	432	US-09-172-528-4	Sequence 4, Appli
19	472.5	28.0	432	US-09-318-199-4	Sequence 4, Appli
20	472.5	28.0	432	US-09-503-579-4	Sequence 4, Appli
21	469.5	27.8	308	US-08-937-466-2	Sequence 2, Appli
22	469.5	27.8	308	US-09-172-528-2	Sequence 2, Appli
23	469.5	27.8	308	US-09-318-199-2	Sequence 2, Appli
24	469.5	27.8	308	US-09-503-579-2	Sequence 2, Appli
25	466.5	27.6	310	US-09-743-847-5	Sequence 5, Appli
26	447.5	26.5	307	US-09-743-847-3	Sequence 3, Appli
27	440	26.0	293	US-09-501-558-4	Sequence 4, Appli

28	439	26.0	306	5	PCT-US94-09799-1	Sequence 1, Appli
29	424	25.1	307	2	US-08-807-861A-56	Sequence 56, Appl
30	424	25.1	307	3	US-09-210-681-56	Sequence 56, Appl
31	424	25.1	307	3	US-08-946-719A-56	Sequence 56, Appl
32	424	25.1	307	4	US-09-547-983-56	Sequence 56, Appl
33	404.5	23.9	275	4	US-09-808-457-4	Sequence 4, Appli
34	404.5	23.9	275	4	US-09-423-410-6	Sequence 6, Appli
35	396.5	23.5	303	1	US-08-518-878B-37	Sequence 37, Appl
36	396.5	23.5	303	1	US-08-294-522B-36	Sequence 36, Appl
37	396.5	23.5	303	2	US-08-807-861A-37	Sequence 37, Appl
38	396.5	23.5	303	2	US-08-470-868A-37	Sequence 37, Appl
39	396.5	23.5	303	3	US-09-210-681-37	Sequence 37, Appl
40	396.5	23.5	303	3	US-08-946-719A-37	Sequence 37, Appl
41	396.5	23.5	303	4	US-09-547-983-37	Sequence 37, Appl
42	376.5	22.3	256	2	US-08-937-466-6	Sequence 6, Appli
43	376.5	22.3	256	2	US-09-172-528-6	Sequence 6, Appli
44	376.5	22.3	256	3	US-09-318-199-6	Sequence 6, Appli
45	376.5	22.3	256	3	US-09-503-579-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2

Query Match		33.1%;	Score 560;	DB 4;	Length 291;
Best Local Similarity		39.0%;	Pred. No. 4.4e-52;		
Matches 115;		Conservative 62;	Mismatches 104;	Indels 14;	Gaps 4;
QY	23	FLISGCAATVAELATPPLDLTKRLQMQGEAALRLGDGARESPYRGVMTALGIIEEE	82		
DB	9	FVYGGASITABECGTFPDLTKRLIQQT-----NDAKFKIRYRGLHALVRIGREE	63		
QY	83	GFLLKMQGVTPAIYRHVYSGGRMVTYEHRLREVFKSDEHYPLWKSVTGMAGVIGQ	142		
DB	64	GLKALYSGIAPAMLRQASVYTKIGTYQSLKRLFIERPEDETLP1--NVICGLSGVISS	121		
QY	143	FLANPTDLVKVQOMEGKLECKPLRFVGVHFAKILAEGGIRGLWAGVWPNQRAAL	202		
DB	122	TIANPTDLVKIRMQAO--SNTIQG-----GMIGNFMNIYQOEGTRGLWKGVSUTAQAAL	174		
QY	203	VNMGDLITVDTVGHVLTPLNTPLDNTMTHTGLSLCSGLVASILGTTPADVTKSRIMNOPRD	262		
DB	175	VVGVELPVVDITKHLILSLGMDTVYTHFLSSFTCLAGALASNPVDVVRTRMMQORVL	234		
QY	263	KQGRGLLYKSSDCLIQAVQGGFMSLYKGFIPSWLRMTFWSMVFWLTYSKIREM	317		
DB	235	RDGRCSGYTGLDCLIQTKWNEGFALYKGFWPNWLRGLPWNIIFFVTYEQKKL	289		

RESULT 2
US-09-743-847-2
; Sequence 2, Application US/09743847

```
; Patent No. 6602694
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108_0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-847-2

Query Match 33.0%; Score 557.5; DB 4; Length 290;
Best Local Similarity 39.9%; Pred. No. 8.1e-52;
Matches 118; Conservative 63; Mismatches 98; Indels 17; Gaps 5;

Qy 23 FLISGCAATVAELATPFLDLTKRLQMGGAALRLGDGAREAPYRGWRTALGIIEEE 82
Db 9 FVYGGSLASIVAEFGTFPVDLTKRLQVQGSIDARF-----KEIKYRGMPHALFRICKEE 63

Qy 83 GFLKLMQGVTPAIRVHVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVGGMMAGVIGQ 142
Db 64 GVLALYSGIAPALLRQASGTIKIGIYQSLKRLFVERLEDE--TLINMICGVVGVSS 121

Qy 143 FLANPTDLVKVQMGEGKRLGKPLFRFG-VHFAFAKILAEGGIRGLWAGVVPNIQRAA 201
Db 122 TIANPTDLVKIRMQAQS-----LFQSGMIGSFIDYIQEGTRGLWGVVPTAQRAA 173

Qy 202 LVNMGDLTYYTVKHVILVNTPLEDNIMTHGLSGLVASILGTPADVIKSRIMNQR 261
Db 174 IVGVGELPVVDITKHLILSGMMGDTILTHFVSSFTCGLAGALASNPVDVTRMMNQ-R 232

Qy 262 DKQGRGLLYKSSDCLIQAVQGGFMSLYKGLPWSLMTWPMVFWLTVEKIREM 317
Db 233 AIVGHVDLYKGTVDGILKMKWKHEGFFALYKGFNPWNLRLGPNWLIIFITTEYQLKRL 288

RESULT 3
US-09-482-273-118
; Sequence 118, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 118
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE

; LOCATION: (335)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-482-273-118

Query Match 33.0%; Score 557.5; DB 4; Length 335;
Best Local Similarity 39.9%; Pred. No. 1e-51;
Matches 118; Conservative 63; Mismatches 98; Indels 17; Gaps 5;

Qy 23 FLISGCAATVAELATPFLDLTKRLQMGGAALRLGDGAREAPYRGWRTALGIIEEE 82
Db 53 FVYGGSLASIVAEFGTFPVDLTKRLQVQGSIDARF-----KEIKYRGMPHALFRICKEE 107

Qy 83 GFLKLMQGVTPAIRVHVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVGGMMAGVIGQ 142
Db 108 GVLALYSGIAPALLRQASGTIKIGIYQSLKRLFVERLEDE--TLINMICGVVGVSS 165

Qy 143 FLANPTDLVKVQMGEGKRLGKPLFRFG-VHFAFAKILAEGGIRGLWAGVVPNIQRAA 201
Db 166 TIANPTDLVKIRMQAQS-----LFQSGMIGSFIDYIQEGTRGLWGVVPTAQRAA 217

Qy 202 LVNMGDLTYYTVKHVILVNTPLEDNIMTHGLSGLVASILGTPADVIKSRIMNQR 261
Db 218 IVGVGELPVVDITKHLILSGMMGDTILTHFVSSFTCGLAGALASNPVDVTRMMNQ-R 276

Qy 262 DKQGRGLLYKSSDCLIQAVQGGFMSLYKGLPWSLMTWPMVFWLTVEKIREM 317
Db 277 AIVGHVDLYKGTVDGILKMKWKHEGFFALYKGFNPWNLRLGPNWLIIFITTEYQLKRL 332

RESULT 4
US-10-001-051B-2
; Sequence 2, Application US/10001051B
; Patent No. 6670138
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Mirella
; APPLICANT: Shamloo, Mehrdad
; APPLICANT: McFarland, K.C.
; APPLICANT: Chin, Daniel
; APPLICANT: Wielech, Tadeusz
; APPLICANT: Melcher, Thorsten
; APPLICANT: AGY Therapeutics, Inc.
; TITLE OF INVENTION: METHODS OF DIAGNOSING , PREVENTING AND TREATING
; FILE REFERENCE: 019488-003010US
; CURRENT APPLICATION NUMBER: US/10/001,051B
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/244,946
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Any animal
; OTHER INFORMATION: source, typically mammalian, most typically human
; US-10-001-051B-2

Query Match 28.2%; Score 476.5; DB 4; Length 309;
Best Local Similarity 34.4%; Pred. No. 5e-43;
Matches 104; Conservative 66; Mismatches 111; Indels 21; Gaps 6;

Qy 18 PRAS-KFLISGCAATVAELATPFLDLTKRLQMGGAALRLGDG---ARESAPYRGWVR 73
Db 11 PTATVKFLGAGTAACIADLITPDLDTAKVRLQIGES-----QGFVRATASAQYRGVMG 64

Qy 74 TALGIIIEEGFLKMQGVTPAIRVHVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVG 133
Db 65 TILTVRTGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ--FYTKGEHASIGSRLLA 122

Qy 134 GMMAGVIGFLANPTDLVKVQMGEGKRLGKPLFRFGVHFAFAKILAEGGIRGLWAG 193
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Db 123 GSTTGALAVAAQPTDVVKVFOAQR---AGGRRYQSTVNAYKTIAREEGRGLWKGT 179

QY 194 VPMQRAALVNMGDLTYDTVVKHYLVNTPLEINIMTHGLSSLCGLVASILGTTPADVIK 253

Db 180 SPVNARNAIVNCAELTYDILKALKANLMTDLPCHFISAFGAGFCITVIASPDVVK 239

QY 254 SRIMNPRDKQGRGLYKSTDCILQAVQGEFMSLYKGLPSWLRMTWMSVFWLTVEK 313

Db 240 TRYMSALGQ-----YSSAGHCALTWLQEGPRAPYKGFPMPSFLRLGWSNVVNFVTEQ 293

QY 314 IR 315

Db 294 LK 295

RESULT 5

US-09-142-565-2

Sequence 2, Application US/09142565A

Patent No. 6187560

GENERAL INFORMATION:

APPLICANT: Lee James Beeley

APPLICANT: Kelly Paine

APPLICANT: Robert James

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GH-30002

CURRENT APPLICATION NUMBER: US/09/142,565A

CURRENT FILING DATE: 1999-06-30

EARLIER APPLICATION NUMBER: 9704551.2

EARLIER FILING DATE: 1997-03-05

EARLIER APPLICATION NUMBER: 9705614.7

EARLIER FILING DATE: 1997-03-18

EARLIER APPLICATION NUMBER: 97305305.1

EARLIER FILING DATE: 1997-07-16

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 312

TYPE: PRT

ORGANISM: HOMO SAPIEN

US-09-142-565-2

Query Match 28.1%; Score 475.5; DB 3; Length 312;

Best Local Similarity 35.8%; Pred. No. 6.5e-43;

Matches 113; Conservative 59; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTRLQOGE---AALARLGDGARESPYRGMTAL 76

Db 14 AVKFLGAGTAACPADLVTFPLDTAKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66

QY 77 GIIEEGFLKMQGVTPAIYRHHVYSGRMVTVYHLREVVFGESEDEHYPLWKSIVGGMM 136

Db 67 TWRTGEGPCSPYNGLVAGLQRMFSASIRIGLVDVKQVTPKQAD-NSSLTRILAGCT 125

QY 137 AGVIGQFLANPTDLVKVQMQE---GKRKLEGLRFRGVHAFKILAEGLRGIRLWAGW 193

Db 126 TGAMAVTCAQPTDVVKVRFQASIHGLGFSRDRK---YSGTMDAVRTIAREEGVRLWKGT 182

QY 194 VPMQRAALVNMGDLTYDTVVKHYLVNTPLEINIMTHGLSSLCGLVASILGTTPADVIK 253

Db 183 LPNIMRNAIVNCAEVVTDILKEKLDYHLLTDFPCHFVSFAFGAGFCATVWASPDVVK 242

QY 254 SRIMNPRDKQGRGLYKSTDCILQAVQGEFMSLYKGLPSWLRMTWMSVFWLTVEK 313

Db 243 TRYMSPPGO-----YFSPLDCKMIKMWAOEGPTAFYKGTTPSFLRLGWSNVVNFVTEQ 296

QY 314 IR-----EMSGVSPF 323

Db 297 LKRALMKVQMLRESPP 312

RESULT 6

US-09-808-457-2

Sequence 2, Application US/09808457

Patent No. 6608038

GENERAL INFORMATION:

APPLICANT: Boettcher, Brian

APPLICANT: Caplan, Shari

APPLICANT: Kaleko, Michael

APPLICANT: Connelly, Shelia

APPLICANT: Desai, Urvi

APPLICANT: Slosberg, Eric

TITLE OF INVENTION: Methods and Compositions For Treatment of Diabetes and Related Conditions Via Gene Therapy

FILE REFERENCE: 4-31353A/USN

CURRENT APPLICATION NUMBER: US/09/808,457

CURRENT FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/XXX,XXX

PRIOR FILING DATE: 2000-03-15

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 312

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Protein UCP3L

US-09-808-457-2

Query Match 28.1%; Score 475.5; DB 4; Length 312;

Best Local Similarity 35.8%; Pred. No. 6.5e-43;

Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTRLQOGE---AALARLGDGARESPYRGMTAL 76

Db 14 AVKFLGAGTAACPADLVTFPLDTAKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66

QY 77 GIIEEGFLKMQGVTPAIYRHHVYSGRMVTVYHLREVVFGESEDEHYPLWKSIVGGMM 136

Db 67 TWRTGEGPCSPYNGLVAGLQRMFSASIRIGLVDVKQVTPKQAD-NSSLTRILAGCT 125

QY 137 AGVIGQFLANPTDLVKVQMQE---GKRKLEGLRFRGVHAFKILAEGLRGIRLWAGW 193

Db 126 TGAMAVTCAQPTDVVKVRFQASIHGLGFSRDRK---YSGTMDAVRTIAREEGVRLWKGT 182

QY 194 VPMQRAALVNMGDLTYDTVVKHYLVNTPLEINIMTHGLSSLCGLVASILGTTPADVIK 253

Db 183 LPNIMRNAIVNCAEVVTDILKEKLDYHLLTDFPCHFVSFAFGAGFCATVWASPDVVK 242

QY 254 SRIMNPRDKQGRGLYKSTDCILQAVQGEFMSLYKGLPSWLRMTWMSVFWLTVEK 313

Db 243 TRYMSPPGO-----YFSPLDCKMIKMWAOEGPTAFYKGTTPSFLRLGWSNVVNFVTEQ 296

QY 314 IR-----EMSGVSPF 323

Db 297 LKRALMKVQMLRESPP 312

RESULT 7

US-09-423-410-4

Sequence 4, Application US/09423410

Patent No. 6620594

GENERAL INFORMATION:

APPLICANT: Giacobino, Jean-Paul

APPLICANT: Muzzin, Patrick

APPLICANT: Boss, Olivier

TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3

FILE REFERENCE: 4-30353/A

CURRENT APPLICATION NUMBER: US/09/423,410

CURRENT FILING DATE: 1999-11-04

EARLIER APPLICATION NUMBER: PCT/EP98/02645

EARLIER FILING DATE: 1998-05-05

EARLIER APPLICATION NUMBER: 1072/97

EARLIER FILING DATE: 1997-05-07

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Protein UCP3L
; US-09-423-410-4

Query Match      28.1%; Score 475.5; DB 4; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTLQMGQE---AALARLGDGARESAPYRGVMRTAL 76
Db 14 AVKFLGAGTAACTADLVTFPLDTAKVRLQIQENQAQVQIARL-----VQYRGVLGTL 66

QY 77 GIIEBEGFLKMQGVTPAIRVHVYSGRMVYVHLREVFGKSEDEHYPLWKSIVIGMM 136
Db 67 TMRTEGPCSPYNGVLVAGLQRMFSFASIRIGLYDSVKQVYTPKGAD-NSSLTTRILAGCT 125

QY 137 AGVIGQFLANPTDLVKVQMGME---GKRLEGKPLRFRGVHHAFAKILAEGGIRGLWAGW 193
Db 126 TGAWAVTCAQPTDVVKRFOAFQSIHLGSPSRDK---YSGTMDAYRTIAREEGVRLWKGT 182

QY 194 VPNIQRAALVNMGDLTYYTVKHVYLVNTPLEDNIMTHGLSSCLSGLVASILGTPADVIK 253
Db 183 LPNIMRNAIVNCAEVYTDILKEKLLDYHLLTDNFPCHFFVSAGAGFCATVVASPVDVVK 242

QY 254 SRIMNPRDKQGRGLLYKSTDCLIQAVQEGPMISLYKGLPDLPSLWRLMTPMSVFWLTYEK 313
Db 243 TRYMNSPPGQ-----YFSLDCMIKMWAOEGPTAFYKGFPTSPFLRLGSMNVVMFVTEQ 296

QY 314 IR-----EMSGVSPP 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 8
US-09-743-847-4
; Sequence 4, Application US/09743847
; Patent No. 6602694
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108 .0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-847-4

Query Match      28.0%; Score 473.5; DB 4; Length 309;
Best Local Similarity 34.4%; Pred. No. 1e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLLSGCAATVAELATFPDLTKTLQMGQAALRLGDG---ARESAPYRGVMR 73
Db 11 PTATVKEFLGAGTAACTADLVTFPLDTAKVRLQIQES-----QGPVRAVASQYRGVMG 64

QY 74 TALGIIEBEGFLKMQGVTPAIRVHVYSGRMVYVHLREVFGKSEDEHYPLWKSIVIG 133
Db 65 TILTMVTEGPRSLYNGVLVAGLQRMFSFASVRIGLYDSVKQ--FYTKGSEHAGISGRLLA 122

QY 134 GMVAGVIGQFLANPTDLVKVQMGMEGKRLEGKPLRFRGVHHAFAKILAEGGIRGLWAGW 193
Db 113 GSTTGALAVAVAQPTDVVKRFOAQAR---AGGRRYQSTVNAVYKTIAREEGVRLWKGT 169

; LENGTH: 312
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Protein UCP3L
; US-09-423-410-4

Query Match      28.1%; Score 475.5; DB 4; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTLQMGQE---AALARLGDGARESAPYRGVMRTAL 76
Db 14 AVKFLGAGTAACTADLVTFPLDTAKVRLQIQENQAQVQIARL-----VQYRGVLGTL 66

QY 77 GIIEBEGFLKMQGVTPAIRVHVYSGRMVYVHLREVFGKSEDEHYPLWKSIVIGMM 136
Db 67 TMRTEGPCSPYNGVLVAGLQRMFSFASIRIGLYDSVKQVYTPKGAD-NSSLTTRILAGCT 125

QY 137 AGVIGQFLANPTDLVKVQMGME---GKRLEGKPLRFRGVHHAFAKILAEGGIRGLWAGW 193
Db 126 TGAWAVTCAQPTDVVKRFOAFQSIHLGSPSRDK---YSGTMDAYRTIAREEGVRLWKGT 182

QY 194 VPNIQRAALVNMGDLTYYTVKHVYLVNTPLEDNIMTHGLSSCLSGLVASILGTPADVIK 253
Db 183 LPNIMRNAIVNCAEVYTDILKEKLLDYHLLTDNFPCHFFVSAGAGFCATVVASPVDVVK 242

QY 254 SRIMNPRDKQGRGLLYKSTDCLIQAVQEGPMISLYKGLPDLPSLWRLMTPMSVFWLTYEK 313
Db 243 TRYMNSPPGQ-----YFSLDCMIKMWAOEGPTAFYKGFPTSPFLRLGSMNVVMFVTEQ 296

QY 314 IR-----EMSGVSPP 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 8
US-09-743-847-4
; Sequence 4, Application US/09743847
; Patent No. 6602694
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108 .0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-847-4

Query Match      28.0%; Score 473.5; DB 4; Length 309;
Best Local Similarity 34.4%; Pred. No. 1e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLLSGCAATVAELATFPDLTKTLQMGQAALRLGDG---ARESAPYRGVMR 73
Db 11 PTATVKEFLGAGTAACTADLVTFPLDTAKVRLQIQES-----QGPVRAVASQYRGVMG 64

QY 74 TALGIIEBEGFLKMQGVTPAIRVHVYSGRMVYVHLREVFGKSEDEHYPLWKSIVIG 133
Db 65 TILTMVTEGPRSLYNGVLVAGLQRMFSFASVRIGLYDSVKQ--FYTKGSEHAGISGRLLA 122

QY 134 GMVAGVIGQFLANPTDLVKVQMGMEGKRLEGKPLRFRGVHHAFAKILAEGGIRGLWAGW 193
Db 113 GSTTGALAVAVAQPTDVVKRFOAQAR---AGGRRYQSTVNAVYKTIAREEGVRLWKGT 169
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194 VPNIQRAALVNMGLTYYDTYVVKHYLVNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253
 170 SPVARNAINVCAELTYDLIKDALLKANLMTDLPCHFTSAFGAGCTTIVIASPVDVVK 229
 254 SRIMNQPRDKQGRGLLYKSTDCLIQAVQEGGFMSSLYKGLPRLWMTWPMVMFWLTYEK 313
 230 TRYMNSALGO-----YSSAGHCALTWLOKEGPRAFYKGFMPFLRLGSMNVVMFVTEYQ 283
 314 IR 315
 284 LK 285

RESULT 10
 US-08-470-868A-56
 ; Sequence 56, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66441 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-470-868A-56

Query Match 28.0%; Score 472.5; DB 2; Length 299;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;
 18 PRAS-KFLSLGCAATVAELATPDLTKRLQWQGEAALRLDGG---ARESPYRGVMR 73
 1 PTATVFLGAGTAACTADLTTPDLTKAVRLQIQGES-----QGPVATVSAQYRGVMG 54
 74 TALGIIEEGFLKLMQGVTPAIYRVHYVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVG 133
 55 TILTVRTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ--FYTKGSEHASIGSRLLA 112
 134 GMMAGVIGQFLANPTDLVKVQWQMEGRKLEKPLFRGVHHAFAKILAEAGGIRGLWAGW 193
 113 GSTTGALAVAVAQPTDVVKRFQAQAR---AGGRRYQSTVNAVYKTIAREEGFRGLWKGT 169
 194 VPNIQRAALVNMGLTYYDTYVVKHYLVNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253

170 SPVARNAINVCAELTYDLIKDALLKANLMTDLPCHFTSAFGAGCTTIVIASPVDVVK 229
 254 SRIMNQPRDKQGRGLLYKSTDCLIQAVQEGGFMSSLYKGLPRLWMTWPMVMFWLTYEK 313
 230 TRYMNSALGO-----YSSAGHCALTWLOKEGPRAFYKGFMPFLRLGSMNVVMFVTEYQ 283
 314 IR 315
 284 LK 285

RESULT 11
 US-08-518-878B-51
 ; Sequence 51, Application US/08518878B
 ; Patent No. 5702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/518,878B
 ; FILING DATE: 23-AUG-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-036
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-518-878B-51

Query Match 28.0%; Score 472.5; DB 1; Length 309;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;
 18 PRAS-KFLSLGCAATVAELATPDLTKRLQWQGEAALRLDGG---ARESPYRGVMR 73
 11 PTATVFLGAGTAACTADLTTPDLTKAVRLQIQGES-----QGPVATVSAQYRGVMG 64
 74 TALGIIEEGFLKLMQGVTPAIYRVHYVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVG 133
 65 TILTVRTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ--FYTKGSEHASIGSRLLA 122
 134 GMMAGVIGQFLANPTDLVKVQWQMEGRKLEKPLFRGVHHAFAKILAEAGGIRGLWAGW 193
 123 GSTTGALAVAVAQPTDVVKRFQAQAR---AGGRRYQSTVNAVYKTIAREEGFRGLWKGT 179
 194 VPNIQRAALVNMGLTYYDTYVVKHYLVNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253
 180 SPVARNAINVCAELTYDLIKDALLKANLMTDLPCHFTSAFGAGCTTIVIASPVDVVK 229
 254 SRIMNQPRDKQGRGLLYKSTDCLIQAVQEGGFMSSLYKGLPRLWMTWPMVMFWLTYEK 313

Db 240 TRYNSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFPSFLRGLSNVWVWFVYEQ 293

Qy 314 IR 315

Db 294 LK 295

RESULT 12

US-08-807-861A-51
 ; Sequence 51, Application US/08807861A
 ; Patent No. 5853975
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 ; TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/807,861A
 ; FILING DATE: 26-FEB-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/518,878
 ; FILING DATE: 23-AUG-1995
 ; APPLICATION NUMBER: US 08/470,868
 ; FILING DATE: 06-JUN-1995
 ; APPLICATION NUMBER: US 08/294,522
 ; FILING DATE: 23-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-066
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-807-861A-51

Query Match 28.0%; Score 472.5; DB 2; Length 309;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

Qy 18 PRAS-KFLSSGCAATVAELATFPDLTKTRLOMQGEAALARLDG---ARESAPYRGWVR 73

Db 11 PTATVKFLGAGTAACIADLTTFPLDTAKVRLQIGES-----QGPVRATVSAQYRGVNG 64

Qy 74 TALGIIEEGFLKMGQVTPAIYRHVYSGGRMVTYHLREVVFGESEDEHYPLWKSIVG 133

Db 65 TILTWRTGEPRLYNGLVAGLQRMQSFASVRIGLYDSVKQ---FYTKESEHASIGSRLLA 122

Qy 134 GNMAGVIGQFLANPTDLVKVQMQMEGKRLKGLKPLFRGVHFAKILAEAGGIRGLWAGW 193

Db 123 GSTTGALAVAVAQPTDVVKVRFQAR---AGGRRYQSTVNAYKTIAREEGFRGLWKGT 179

Qy 194 VPNIQRAALVNMGDLTYDVTVKHYLVNLTPLDNTMTHGLSLCSGLVASILGTPADVIK 253

Db 180 SPNVARNAINVCAELVYDILKDALKANLMTDDLPCHFTSAFGAGFCTTVIASPVDVVK 239

Qy 254 SRIMNQPRDKQGRGLLYKSTDCLIQAVQGEGFMSLYKGLFPLSWLRMTWMSVFWLTYYEK 313

Db 240 TRYNSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFPSFLRGLSNVWVWFVYEQ 293

Qy 314 IR 315

Db 294 LK 295

RESULT 13

US-08-470-868A-51
 ; Sequence 51, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66441 PENNIE
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-470-868A-51

Query Match 28.0%; Score 472.5; DB 2; Length 309;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

Qy 18 PRAS-KFLSSGCAATVAELATFPDLTKTRLOMQGEAALARLDG---ARESAPYRGWVR 73

Db 11 PTATVKFLGAGTAACIADLTTFPLDTAKVRLQIGES-----QGPVRATVSAQYRGVNG 64

Qy 74 TALGIIEEGFLKMGQVTPAIYRHVYSGGRMVTYHLREVVFGESEDEHYPLWKSIVG 133

Db 65 TILTWRTGEPRLYNGLVAGLQRMQSFASVRIGLYDSVKQ---FYTKESEHASIGSRLLA 122

Qy 134 GNMAGVIGQFLANPTDLVKVQMQMEGKRLKGLKPLFRGVHFAKILAEAGGIRGLWAGW 193

Db 123 GSTTGALAVAVAQPTDVVKVRFQAR---AGGRRYQSTVNAYKTIAREEGFRGLWKGT 179

Qy 194 VPNIQRAALVNMGDLTYDVTVKHYLVNLTPLDNTMTHGLSLCSGLVASILGTPADVIK 253

Db 180 SPNVARNAINVCAELVYDILKDALKANLMTDDLPCHFTSAFGAGFCTTVIASPVDVVK 239

QY 254 SRIMQPRDKQGRGLLYKSDCLIOAQVQEGFMSLYKGFLPSWLRLMTWMSVFWLTYEK 313
Db 240 TRYMSALQ-----YSSAGHCALTMLOKEGPRAFYKGFMPFSLRGLGSNNVVMFVTEYQ 293
QY 314 IR 315
Db 294 LK 295

RESULT 14
US-09-210-681-51
; Sequence S1, Application US/09210681
; Patent No. 6057109
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/807,861
; FILING DATE: 26-FEB-1997
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-09-210-681-51

Query Match 28.0%; Score 472.5; DB 3; Length 309;
Best Local Similarity 34.4%; Pred. No. 1.3e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLISGCAATVAELATFPLDTKTRIQMOGEAALARLGDG---ARESAPYRGMVR 73
Db 11 PTATVKFLGAGTAACTADLITFPLDTAKVRLQIGSES-----QGPRVATVSAQYRGVNG 64
QY 74 TALGIIEEGFLKMGVTPAIRVHVYGGRMVTVYHLRVVFGKSEDEHYPLWKSIVIG 133
Db 65 TILTWRTTGPRLSYNLVAGLQRMSPASVRIGLYDSVKQ--FYTKGSEHASIGSRLLA 122
QY 134 GMMAGVIGOFLANPTDLVKVQMGEKRLKGLKPLFRGVVHAFKILAEGGIRGLWAGW 193

Db 123 GSTTGALAVAVAQPTDVKVRFOAQR---AGGRRYQSTVNAYKTIAREEGRGLWKGT 179
QY 194 VFNIORAALVNMGDLTTTYDTVKHYLVNTPLEBNDINMTHGLSSICSLGSLVASILGTADVIK 253
Db 180 SPVARNAIVNCALVTVYDLIKDALLKANLMTDDLPCFTSAFGAGCFTTVIASPVDVVK 239
QY 254 SRIMQPRDKQGRGLLYKSDCLIOAQVQEGFMSLYKGFLPSWLRLMTWMSVFWLTYEK 313
Db 240 TRYMSALQ-----YSSAGHCALTMLOKEGPRAFYKGFMPFSLRGLGSNNVVMFVTEYQ 293
QY 314 IR 315
Db 294 LK 295

RESULT 15
US-08-946-719A-51
; Sequence S1, Application US/08946719A
; Patent No. 6121017
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,719A
; FILING DATE: 8-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/807,861
; FILING DATE: 26-FEB-1997
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-08-946-719A-51

Query Match 28.0%; Score 472.5; DB 3; Length 309;
Best Local Similarity 34.4%; Pred. No. 1.3e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLISGCAATVAELATFPLDTKTRIQMOGEAALARLGDG---ARESAPYRGMVR 73
Db 11 PTATVKFLGAGTAACTADLITFPLDTAKVRLQIGSES-----QGPRVATVSAQYRGVNG 64

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QY 74 TALGIIIEEGFLKMQGVTPIYRHVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS VIG 133
Db 65 TILTMVTEGPRSLYNGLVAGLQOMSFASVRIGLYDSVKQ--FYTKGSEHAGISGRLLA 122
QY 134 GMMAGVIGQFLANPTDLVKVQMOMEGKRLKLEKPLRPGVHHAFAPAKILAEGGIRGLWAGW 193
Db 123 GSTTGALAVAVAQFTDVVKVRFQOAR---AGGRRYQSTVNAYKTIAREEGFRGLWKG 179
QY 194 VPNIQRAALVNMGDLTTYDTVKHYLVLTNTPLEDNIMTHGLSLCSGLVASILGTADVIK 253
Db 180 SPNVARNAINVCAELVTYDUIKALLKANLMTDLPCHFTSAFGAGFCITTVIASPVDVVK 239
QY 254 SRIMNQRDKQGRLLYKSSDCLIOAVQGEGFMSLYKGFPLPSWLMTWMSVFWLTYEK 313
Db 240 TRYMSALGO-----YSSAGHCALTWLQKEGPRAFYKGFMPSPFLRLGSMNVVMFVTEQ 293
QY 314 IR 315
Db 294 LK 295

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Search completed: September 24, 2004, 03:58:35
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2004, 03:44:32 ; Search time 49 Seconds
(without alignments)
634.079 Million cell updates/sec

Title: US-09-397-342C-1

Perfect score: 1690

Sequence: 1 MSVPSEERLLPLTQWRPA.....SMVFWLTYKIREMSGVSFP 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	777	46.0	343	T15253	hypothetical prote
2	667.5	39.5	305	H86274	F7A19.22 protein -
3	551.5	32.6	325	JC7553	brain mitochondria
4	546.5	32.3	306	T47570	uncoupling protein
5	538.5	31.9	306	T07793	uncoupling protein
6	537.5	31.8	306	T52024	uncoupling protein
7	475.5	28.1	312	JC5522	uncoupling protein
8	455.5	27.0	313	D84813	hypothetical prote
9	447.5	26.5	307	G01858	uncoupling protein
10	434.5	25.7	306	A32446	uncoupling protein
11	432.5	25.6	313	T05577	uncoupling protein
12	425	25.1	307	S34268	uncoupling protein
13	424	25.1	306	A31106	mitochondrial unco
14	422	25.0	307	A26294	uncoupling protein
15	419.5	24.8	288	S03603	uncoupling protein
16	399.5	23.6	314	A36305	2-oxoglutarate/mal
17	387.5	22.9	314	A56650	2-oxoglutarate car
18	381.5	22.6	323	T25459	hypothetical prote
19	366.5	21.7	290	S44091	oxoglutarate/malat
20	345	20.4	282	T49828	probable dicarboxy
21	338	20.0	298	S51351	hypothetical prote
22	333.5	19.7	324	S25357	mitochondrial unco
23	332	19.6	297	T07405	oxoglutarate/malat
24	299.5	17.7	302	S65042	2-oxoglutarate/mal
25	298	17.6	331	T51899	probable 2-oxoglut
26	296.5	17.5	302	S65040	2-oxoglutarate/mal
27	288	17.0	320	T37603	probable oxaloacet
28	272.5	16.1	309	T48156	hypothetical prote
29	269.5	15.9	352	T01729	mitochondrial solu

30	259	15.3	702	2	T16533	hypothetical prote
31	255	15.1	332	2	T47703	Ca-dependent solut
32	251.5	14.9	386	2	S17917	ADP,ATP carrier pr
33	249.5	14.8	386	2	S21974	ADP,ATP carrier pr
34	248	14.7	415	2	T48171	hypothetical prote
35	247	14.6	381	2	T51158	hypothetical prote
36	246.5	14.6	298	1	S03894	ADP,ATP carrier pr
37	245.5	14.5	298	2	B43646	ADP,ATP carrier pr
38	245.5	14.5	313	1	XWNC	ADP,ATP carrier pr
39	245	14.5	308	1	S30259	ADP,ATP carrier pr
40	244	14.4	387	2	S14876	ADP,ATP carrier pr
41	243.5	14.4	379	2	T04608	probable mitochond
42	242	14.3	348	2	D84798	ADP,ATP carrier pr
43	241	14.3	387	2	S16568	ADP,ATP carrier pr
44	238.5	14.1	298	1	A44778	ADP,ATP carrier pr
45	237.5	14.1	307	2	A36582	ADP,ATP carrier pr

ALIGNMENTS

RESULT 1

T15253

hypothetical protein K07B1.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000

C;Accession: T15253

R;Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, May 1997

A;Description: The sequence of C. elegans cosmid K07B1.

A;Reference number: Z18317

A;Accession: T15253

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-343 <PAU>

A;Cross-references: EMBL:AF003384; NID:g2088817; PID:g2088821; PIDN:AAB54239.1; CSPDB:GN

A;Experimental source: strain Bristol N2; clone K07B1

C;Genetics:

A;Gene: CBSP:K07B1.3

A;Map position: 5

A;Introns: 81/1; 131/3; 236/3; 279/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 46.0%; Score 777; DB 2; Length 343;

Best Local Similarity 46.5%; Pred. No. 1.9e-59;

Matches 154; Conservative 60; Mismatches 85; Indels 32; Gaps 5;

QY 8 ERLPLTQWRPAS-----KPLSGCAATVAELATFPLDLTKTKLQMGGEAALARLGDGAR 63

Db 30 QQVLP-----RTSIYFYFLSCTAALVAETVYPLDITKRLQI-----AR 72

QY 64 ESAPYRG--WVRTALGIIIEEGFLKMGVTPAIVRHVVYSGGRMVTYHLRVVFGKSE 121

Db 73 NKFTKGIMVQVYTDIIRREGAALMTGVAPAITRHYIYTGIRMGAYEQIRLTTNKEV 132

QY 122 DEHYPLWKSIVIGOMAGVICQFLANPTDLVKVQMMEGKRLKGLRFRGVHFAKIL 181

Db 133 EKSPFLWKSMLCGAFSLAQFAASPTDLVKVQMMEGLRRLQKQPLRYTGATDCPSLY 192

QY 182 AEGGIRGLWAGVFNPTQRAALVNMGDLTTYDTVKHVLVNLPTLEDNIMTHGLSSCLGV 241

Db 193 RTQGFGLWGNPCQRAALLNADIATYDSVKHGLIDNFKLKNLTHAVASACAGLA 252

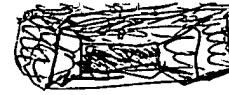
QY 242 ASILGTGPAVIVKIRINMOPDKQGRGLLYKSSP-----DCLLOAVQGEFMSLYKG 292

Db 253 AAIVLPSDVVKTRMMDQIRHELDAAOMHKKNTHVDLYKGVVDYCIKIKNKGFFSLYKG 312

QY 293 FLPSWLRMTFWSMVFWLTYEKIREMSGVSFP 323

Db 313 FLPSYIRMAPWSLTFWVSVEEIRKWTGASSF 343

RESULT 2



Db 183 LPNIMNAIVNCAEVVYDILKSLDYLHLLTNTFCHVFVSAGAGCATVVASPVDDVK 242

QY 254 SRIMNPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGLPSWLRLMTPMWSMFWLTYEK 313

Db 243 TRYNSPPGQ-----YFSLDCMIKXVAQEGTAFYKGTFTPSFLRLGSNNVVMFVTEQ 296

QY 314 IRY-----EMSGVSPF 323

Db 297 LKRALMKVQMLRESPPF 312

RESULT 8

D84613

hypothetical protein At2g22500 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: D84613

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

emus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84613

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-313 <STO>

A:Cross-references: GB:AE002093; NID:g4544443; PIDN:AAD22351.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g22500

A:Map position: 2

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 27.0%; Score 455.5; DB 2; Length 313;

Best Local Similarity 34.7%; Pred. No. 1.1e-31;

Matches 107; Conservative 60; Mismatches 122; Indels 19; Gaps 6;

QY 23 FLLSGCAATVAELATPFLDLTKTRLQMGSA-----ALARLGDGARESAPYR-GMV 72

Db 6 FAEAGTASIVAGCTHPELDLILKVMQLQGSAPIQTNLRPALAFQSTTVNAPPLRVGI 65

QY 73 RTALGIIEEGFLKMQGVTPAIRHVYVYGGRMVTVYHLREVVFVK---SEDEHYPLWK 129

Db 66 GVGSRLIEEGRMALPFGVSATVLRQTLYSTTRMGLY---DIKGEWTDPETKTMPLMK 121

QY 130 SVTGGMWAGVIGQFLANPTDLVKVQMGEKLEKGLRFRGVVHFAFALAEGGIRGL 189

Db 122 KIGAGATAGAIGAAGVGNPDAVMYRMQADGRPLPTDR-RNYKSVLDITQIRGEGVTSL 180

QY 190 WAGVWPNIORAALVNMGDLTDTYDVTKHYLVNLTPLEDNIMTHGLSSLCSGIVASILGTPA 249

Db 181 WRGSSLTINRAMLVTSQLASYSVSKETILEKGLLKOGLGTHVSASFAAGFVASVSNPV 240

QY 250 DVTKSRIMNPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGLPSWLRLMTPMWSMFWL 309

Db 241 DVIKTRVMNM-KVAVGAVPPYKGAVDCAKTKVAEGIMSLYKGFIPVSRQAPFTVVLV 299

QY 310 TYEKIREM 317

Db 300 TLEQVKKL 307

RESULT 9

G01858

uncoupling protein 1, mitochondrial - human

N:Alternate names: UCP1

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000

C:Accession: G01858; S78473; S29141; A60793; A45763

R:Bouillaud, F.

A:Reference number: G08642

A:Accession: G01858

RESULT 13
 A31106
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jul-2000
 C/Accession: A31106
 R/Kozak, L.P.; Britton, J.H.; Korak, U.C.; Wells, J.M.
 J. Biol. Chem. 263, 12274-12277, 1988
 A>Title: The mitochondrial uncoupling protein gene. Correlation of exon structure to tra
 A/Reference number: A31106; MUID:88315014; PMID:3410843
 A/Accession: A31106
 A/Molecule type: DNA; mRNA
 A/Residues: 1-306 <KOZ>
 A/Cross-references: GB:U63418; NID:g1519064; PIDN:AA07367.1; PID:g1519065
 C/Genetics:
 A/Genes: Ucp
 A/Introns: 41/3; 108/1; 175/1; 209/1; 269/2
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: duplication; mitochondrion; transmembrane protein
 F:9-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:109-201/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:208-295/Domain: ADP,ATP carrier protein repeat homology <ACP3>
 Query Match 25.1%; Score 424; DB 2; Length 306;
 Best Local Similarity 30.8%; Pred. No. 5,4e-29;
 Matches 91; Conservative 67; Mismatches 121; Indels 16; Gaps 4;
 QY 22 KFLSGCAATVAELATFPLDITKTLQMOGEAALRGDGAESAPYGMVMTALGIIEE 81
 Db 15 KIFSAGVSACLAADIITFPLDTAKVRLQIQGEGQ-----ASSTIRYKGVLTITTLAKT 67
 QY 82 EGFLLKMQGVTPAIYRHVVYSGRMVTVYHLREVVFVKGSEDEHYPLWKSIVGGMAGVIG 141
 Db 68 EGLPKLYSGLPAGIQRIQSFASLRIGLYDVQVE-YFSSGRETTPASLGNKISAGLMTGGVA 126
 QY 142 QFLANPTDLVKVQMEGRKLEKPLRFRGVHFAFILAEGGIRGLWAGWVFNIOQAA 201
 Db 127 VFIOGPTVEVVKVQMAQS--HLHGKIPRYTGTYNAYRVIAATTESLSTLWKGTTPLNMRNV 184
 QY 202 LVNMGDLTITDVTYKHVLYLNTPLDNIWTHGLSSICSLGSLVASILGTPADVIKSRIMQPR 261
 Db 185 IINCTELVTDLMKGLVNNHILADDPVCHLLSALVAGFTCTLLASPDVVDVVKTRFINSLP 244
 QY 262 DKQGRGLLYKSTDCILQAVQGEFMSLYKGFPLPSWLMRTFWSMVFWLTVEKIRE 316
 Db 245 GQ-----YPSVPSCAMTYTKGPTAFFKGFVASFRLGSMNVIMFVCFEQLKK 293
 RESULT 14
 A26294
 uncoupling protein - rat
 N/Alternate names: UCP
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Feb-2000
 C/Accession: A26294; A29278; S03842; A61566
 R/Bouillaud, F.; Weissenbach, J.; Ricquier, D.
 J. Biol. Chem. 261, 1487-1490, 1986
 A>Title: Complete nucleotide and derived amino acid sequence of cDNA encoding the mitoch
 A/Reference number: A29278; MUID:86232540; PMID:3012461
 A/Accession: A29278
 A/Molecule type: mRNA
 A/Residues: 1-307 <BOU>
 A/Cross-references: GB:M11814; NID:g207556; PIDN:AA119671.1; PID:g207557
 R/Ridley, R.G.; Patel, H.V.; Gerber, G.B.; Morton, R.C.; Freeman, K.B.
 Nucleic Acids Res. 14, 4025-4035, 1986
 A>Title: Complete nucleotide and derived amino acid sequence of cDNA encoding the mitoch
 A/Reference number: A29278; MUID:86232540; PMID:3012461
 A/Accession: A29278
 A/Molecule type: mRNA
 A/Residues: 1-307 <R12>
 A/Cross-references: GB:X03894; GB:M15500; NID:g57446; PIDN:CAA27531.1; PID:g57447
 R/Bouillaud, F.; Raimbault, S.; Ricquier, D.

Biochem. Biophys. Res. Commun. 157, 783-792, 1988
 A>Title: The gene for rat uncoupling protein: complete sequence, structure of primary tra
 A/Reference number: S03842; MUID:89076317; PMID:3202878
 A/Accession: S03842
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-307 <BO2>
 A/Cross-references: EMBL:X12925; NID:g57444; PIDN:CAA311392.1; PID:g57445
 R/Ridley, R.G.; Patel, H.V.; Parfett, C.L.J.; Olynky, K.A.; Reichling, S.; Freeman, K.B.
 Biochem. Res. 6, 87-94, 1986
 A>Title: Immunological detection of cDNA clones encoding the uncoupling protein of brown
 A/Reference number: A61566; MUID:86188126; PMID:2421800
 A/Accession: A61566
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 254-307 <RID>
 C/Comment: The source of this protein was brown adipocyte mitochondria.
 C/Genetics:
 A/Introns: 42/3; 109/1; 176/1; 210/1; 270/2
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: duplication; mitochondrion; transmembrane protein
 F:10-103/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:209-296/Domain: ADP,ATP carrier protein repeat homology <ACP3>
 Query Match 25.0%; Score 422; DB 2; Length 307;
 Best Local Similarity 30.8%; Pred. No. 8.1e-29;
 Matches 91; Conservative 67; Mismatches 121; Indels 16; Gaps 4;
 QY 22 KFLSGCAATVAELATFPLDITKTLQMOGEAALRGDGAESAPYGMVMTALGIIEE 81
 Db 16 KIFSAGVSACLAADIITFPLDTAKVRLQIQGEGQ-----ASSTIRYKGVLTITTLAKT 68
 QY 82 EGFLLKMQGVTPAIYRHVVYSGRMVTVYHLREVVFVKGSEDEHYPLWKSIVGGMAGVIG 141
 Db 69 EGLPKLYSGLPAGIQRIQSFASLRIGLYDVQVE-YFSSGRETTPASLGNKISAGLMTGGVA 127
 QY 142 QFLANPTDLVKVQMEGRKLEKPLRFRGVHFAFILAEGGIRGLWAGWVFNIOQAA 201
 Db 128 VFIOGPTVEVVKVQMAQS--HLHGKIPRYTGTYNAYRVIAATTESLSTLWKGTTPLNMRNV 185
 QY 202 LVNMGDLTITDVTYKHVLYLNTPLDNIWTHGLSSICSLGSLVASILGTPADVIKSRIMQPR 261
 Db 186 IINCTELVTDLMKGLVNNHILADDPVCHLLSALVAGFTCTLLASPDVVDVVKTRFINSLP 245
 QY 262 DKQGRGLLYKSTDCILQAVQGEFMSLYKGFPLPSWLMRTFWSMVFWLTVEKIRE 316
 Db 246 GQ-----YPSVPSCAMTYTKGPTAFFKGFVASFRLGSMNVIMFVCFEQLKK 294
 RESULT 15
 S03603
 uncoupling protein - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Jun-2000
 C/Accession: S03603; S05075
 R/Casteilla, L.; Bouillaud, F.; Forest, C.; Ricquier, D.
 Nucleic Acids Res. 17, 2131, 1989
 A>Title: Nucleotide sequence of a cDNA encoding bovine brown fat uncoupling protein. Hom
 A/Reference number: S03603; MUID:89183626; PMID:2928121
 A/Accession: S03603
 A/Molecule type: mRNA
 A/Residues: 1-288 <CAS>
 A/Cross-references: EMBL:X14064; NID:g1495201; PIDN:CAA32227.1; PID:g1495202
 R/Ricquier, D.
 submitted to the EMBL Data Library, January 1989
 A/Reference number: S05075
 A/Accession: S05075
 A/Molecule type: mRNA
 A/Residues: 1-195,201,'T',203,'RCC',204-288 <RIC>
 A/Cross-references: EMBL:X14064
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: duplication; mitochondrion; transmembrane protein

Search completed: September 24, 2004, 03:57:31
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2004, 21:08:37 ; Search time 44 Seconds
(without alignments)

382.242 Million cell updates/sec

Title: US-09-397-342C-1

Perfect score: 1690

Sequence: 1 MSVPDEERLLPLTORPRA.....SMVFNLTYEKIREMSGVSPF 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1690	100.0	323	1	UCP4_HUMAN
2	557.5	33.0	325	1	UCP5_HUMAN
3	552.5	32.7	325	1	UCP5_MOUSE
4	504.5	29.9	311	1	UCP3_BOVIN
5	480.5	28.4	308	1	UCP3_PIG
6	475.5	28.1	312	1	UCP3_HUMAN
7	474	28.0	311	1	UCP3_CANFA
8	473.5	28.0	308	1	UCP3_MOUSE
9	473.5	28.0	309	1	UCP2_HUMAN
10	473.5	28.0	309	1	UCP2_RAT
11	472.5	28.0	309	1	UCP2_CANFA
12	472.5	28.0	309	1	UCP2_MOUSE
13	472.5	28.0	309	1	UCP2_PIG
14	471.5	27.9	308	1	UCP3_RAT
15	459	27.2	310	1	UCP2_CYPCA
16	442	26.2	310	1	UCP2_BRARE
17	441.5	26.1	307	1	UCP1_HUMAN
18	433.5	25.7	306	1	UCP1_RABIT
19	425	25.1	306	1	UCP1_MESAU
20	424	25.1	306	1	UCP1_MOUSE
21	422	25.0	306	1	UCP1_RAT
22	419.5	24.8	288	1	UCP1_BOVIN
23	399.5	23.6	313	1	M2OM_BOVIN
24	391.5	23.2	313	1	M2OM_MOUSE
25	387.5	22.9	313	1	M2OM_HUMAN
26	376.5	22.3	313	1	M2OM_RAT
27	365	21.6	287	1	DIC_MOUSE
28	363	21.5	287	1	DIC_HUMAN
29	333.5	19.7	324	1	OACI_YEAST
30	259	15.3	702	1	CMCI_CABEL
31	253	15.0	299	1	ODC_HUMAN
32	249.5	14.8	386	1	ADTI_SOLU
33	246.5	14.6	298	1	ADT3_HUMAN

34	246	14.6	382	1	ADT_ORYSA
35	245.5	14.5	298	1	ADT3_BOVIN
36	245.5	14.5	313	1	ADT_NEUCR
37	245	14.5	308	1	ADT_CHLRE
38	244	14.4	387	1	ADT1_MAIZE
39	241	14.3	387	1	ADT2_MAIZE
40	238.5	14.1	298	1	ADT1_HUMAN
41	237.5	14.1	307	1	ADT3_YEAST
42	237.5	14.1	310	1	ODCI_YEAST
43	237.5	14.1	322	1	SFCI_YEAST
44	235.5	13.9	297	1	ADT1_BOVIN
45	234.5	13.9	298	1	ADT1_RAT

ALIGNMENTS

RESULT 1
UCP4_HUMAN STANDARD; PRT; 323 AA.
AC O95847;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DB Mitochondrial uncoupling protein 4 (UCP 4) (UNQ772/PRO1566).
GN UCP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99148824; PubMed=10025957;
RA Mao W., Yu X.X., Zhong A., Li W., Brush J., Sherwood S.W., Adams S.H.,
RA Pan G.;
RT "UCP4, a novel brain-specific mitochondrial protein that reduces
RT membrane potential in mammalian cells.";
RL FEBS Lett. 443:326-330(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.I., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu O., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
CC -I- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE. THUS
CC UNCOUPLING OXIDATIVE PHOSPHORYLATION FROM ATP SYNTHESIS. AS A
CC RESULT, ENERGY IS DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE
CC IN THERMOREGULATORY HEAT PRODUCTION AND METABOLISM IN BRAIN.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -I- TISSUE SPECIFICITY: Found in adult and fetal brain. Present in
CC most of the brain tissues, with low levels in spinal chord, corpus
CC callosum and substantia nigra.
CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -I- SIMILARITY: Contains 3 Solcar repeats.

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 CC -----

DR EMBL; AF110532; AAD16995.1; -
 DR EMBL; AY358711; AAO89951.1; -
 DR GO; GO:0005739; C:mitochondrion; TAS.
 DR GO; GO:0015302; F:uncoupling protein activity; TAS.
 DR GO; GO:0006091; P:energy pathways; TAS.
 DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carri; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS50920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 23 40
 FT TRANSMEM 88 109
 FT TRANSMEM 127 144
 FT TRANSMEM 195 212
 FT TRANSMEM 229 248
 FT TRANSMEM 288 311
 FT REPEAT 21 115
 FT REPEAT 125 217
 FT REPEAT 226 317
 FT DOMAIN 5 8
 SQ SEQUENCE 323 AA; 36064 MW; 4C54A56BB10333ED CRC64;
 Query Match 100.0%; Score 1690; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2.2e-131;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPEEERLLPTQRPFRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
 DB 1 MSVPEEERLLPTQRPFRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
 QY 61 GAREAPYRGVMVTRALGIIEEGFLKVGQVTPAIRHVYSGRMVYTHLREVWFGKS 120
 DB 61 GAREAPYRGVMVTRALGIIEEGFLKVGQVTPAIRHVYSGRMVYTHLREVWFGKS 120
 QY 121 EDEHYPLKWSVIGGMAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHAPAKI 180
 DB 121 EDEHYPLKWSVIGGMAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHAPAKI 180
 QY 181 LAEGGIRGLWAGVNTORALVNNGLDITVDYTKVHLVNLTPLEDMTHGLSSLCGSL 240
 DB 181 LAEGGIRGLWAGVNTORALVNNGLDITVDYTKVHLVNLTPLEDMTHGLSSLCGSL 240
 QY 241 VASILGTTPADVIKSRIMNQPRDKQGRGLYKSSDCLIQAVQGGFMSLYKGFPLPSWLRM 300
 DB 241 VASILGTTPADVIKSRIMNQPRDKQGRGLYKSSDCLIQAVQGGFMSLYKGFPLPSWLRM 300
 QY 301 TPWSMVFWLTYEKIREMSGVSPF 323
 DB 301 TPWSMVFWLTYEKIREMSGVSPF 323
 RESULT 2
 UCPS5 HUMAN STANDARD; PRT; 325 AA.
 AC O95258; Q9HC60; Q9HC61;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Brain mitochondrial carrier protein-1 (BMCP-1) (Mitochondrial
 DE uncoupling protein 5) (UCP 5) (Solute carrier family 25, member 14)
 DE (UNQ791/PRO1682).
 DE SLIC25A14 OR BMCP1 OR UCP5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99069464; PubMed=9852133;
 RA Sanchis D., Fleury C., Chomiki N., Goubert M., Huang Q., Neverova M.,
 RA Gregoire F., Eslick J., Rimbault S., Levi-Meyrueis C., Miroux B.,
 RA Collins S., Seldin M., Richard D., Warden C., Bouillaud F.,
 RA Riquier D.;
 RT "BMCP1, a novel mitochondrial carrier with high expression in the
 RT central nervous system of humans and rodents, and respiration
 RT uncoupling activity in recombinant yeast.";
 RL J. Biol. Chem. 273:34611-34615 (1998).
 RN [2]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RX MEDLINE=20387222; PubMed=10928996;
 RA Yu X.X., Mao W., Zhong A., Schow P., Brush J., Sherwood S.W.,
 RA Adams S.H., Pan G.;
 RT "Characterization of novel UCP5/BMCP1 isoforms and differential
 RT regulation of UCP4 and UCP5 expression through dietary or temperature
 RT manipulation.";
 RL FASEB J. 14:1611-1618 (2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22987296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX Pearce A.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Participates to the mitochondrial proton leak measured
 CC in brain mitochondria.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=UCP5L;
 CC IsoId=O95258-1; Sequence=Displayed;
 CC Name=2; Synonyms=UCP5S;
 CC IsoId=O95258-2; Sequence=VSP_003272;
 CC Name=3; Synonyms=UCP5SI;
 CC IsoId=O95258-3; Sequence=VSP_003272, VSP_003273;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Some expression in
 CC testis and pituitary.
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -!- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch.
 CC -----
 CC EMBL; AF078544; AAD04346.1; -
 CC EMBL; AF155809; AAG29582.1; -
 CC EMBL; AF155810; AAG29583.1; -
 CC EMBL; AF155811; AAG29584.1; -
 CC EMBL; AY358099; AAO88466.1; -
 CC EMBL; AL035423; CAB41251.1; -
 CC EMBL; HGNC:10984; SLC25A14.
 CC MIM; 300242; -
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005739; C:mitochondrion; TAS.
 CC GO; GO:0005386; F:carrier activity; TAS.

QY 143 FLANPTDLVKVQMQEGRKLEKPLFRG-VHFAKILAEAGIRGLWAGVNPQRAA 201
 Db 157 TIANTDVLKIRMAQGS-----LFQSGMIGSFIDYIQOEGTRGLWGVPTAQRAA 208
 QY 202 LVNMGDTLTTVDYTKHYLVNTPLEDNIMTHGLSSCLSGLVASILGTTPADVIKGRIMNQPR 261
 Db 209 IVGVGVELPVYDITKKHLIVSGMLGDTILTHFVSSFTCLGALASNPVDVVRTRMMNQ-R 267
 QY 262 DKQGRGLYKSSDCLTQAVQEGFMSLYKGLPLSMRTMTPWSVFWLTIEKIREM 317
 Db 268 AIVGHVDLYKGTLDGILKMKWKEGFFALYKGFENWLRGLGFNLIFFITTYEQLKRL 323

RESULT 4
 UCP3_BOVIN
 ID UCP3_BOVIN STANDARD; PRT; 311 AA.
 AC 077792; Q9TVAI;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 3 (UCP 3).
 GN UCP3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Stone R.T., Smith T.P.L.;
 RT "Bovine uncoupling protein 3";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE OF 1-274 FROM N.A., AND VARIANT THR-53.
 RA Stone R.T., Rexroad C.E., Smith T.P.L.;
 RT "Bovine UCP2 and UCP3 map to BTAL5";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS. THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
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 CC -----
 DR EMBL; AF092048; AAC61762.1; -
 DR EMBL; AF127030; AAD33339.1; -
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PR00784; MTUNCOUPLING.
 DR PROSITE; PS50920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Polymorphism.
 FT TRANSMEM 11 32 1 (POTENTIAL).
 FT TRANSMEM 77 99 2 (POTENTIAL).
 FT TRANSMEM 120 136 3 (POTENTIAL).
 FT TRANSMEM 183 199 4 (POTENTIAL).
 FT TRANSMEM 217 236 5 (POTENTIAL).

FT TRANSMEM 271 293 6 (POTENTIAL).
 FT REPEAT 11 105 SOLCAR 1.
 FT REPEAT 114 205 SOLCAR 2.
 FT REPEAT 214 299 SOLCAR 3.
 FT DOMAIN 278 300 PURINE NUCLEOTIDE BINDING (BY
 FT SIMILARITY).
 FT VARIANT 53 53 A -> T.
 SQ SEQUENCE 311 AA; 34205 MM; B1A1D26E25650D04 CRC64;
 Query Match 29.9%; Score 504.5; DB 1; Length 311;
 Best Local Similarity 36.7%; Pred. No. 3.8e-34;
 Matches 117; Conservative 61; Mismatches 118; Indels 23; Gaps 7;
 QY 14 TORWPRAS-KFLLSGCAATVAELATPPLDLTKRLQMQGE--AALARLGLGARESAFYRG 70
 Db 7 SERPTTSVKFLAAGTAACFADLLTFLDTAKVRLQIQENQAAL-----AARSAYRG 60
 QY 71 MVRTALGIIEEGFLKLWQGVTPAIYRVVYVSGRMVTVYHRLREVVFVFGKSEDEHYPLWKS 130
 Db 61 VLGTILTMVTRTEGPRSLYSLVAGLQRMQSFASIRIGLYDSVKQFYTPKGS-D-HSSIIR 119
 QY 131 VIGGMAGVIGQFLANPTDLVKVQMQEGRKLEKPLFRGVHFAKILAEAGIRGLW 190
 Db 120 ILAGTTGAMAVTCAQPTDVVKIRFOASMTGLGKN-RKYSGTMDAYRTIARBEVRLW 178
 QY 191 AGWVPNIQRAALVNMGDLTITDVKHYLVNTPLEDNIMTHGLSSCLSGLVASILGTTPAD 250
 Db 179 KGILPNITRNAIVNCGEMVTYDIIEKLLDYHLLTDFNFCFVSAGAGCAILVASPVD 238
 QY 251 VIKSRIMNPRDKQGRGLYKSSDCLTQAVQEGFMSLYKGLPLSMRTMTPWSVFWLT 310
 Db 239 VVKTRYMNSPPGQ-----YHSPFDCMLXWVTQEGPTAFYKGTPTSPFLRLGSMNVVMFVT 292
 QY 311 YEKIR-----EMSGVSPF 323
 Db 293 YEOMKRALMKVQMLRDSPF 311

RESULT 5
 UCP3_PIG
 ID UCP3_PIG STANDARD; PRT; 308 AA.
 AC 097649; Q9XSE6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 3 (UCP 3).
 GN UCP3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=White adipose tissue;
 RA Werner P., Nowaczny K., Neuenschwander S., Strazinger G.;
 RT "Characterization of the porcine uncoupling proteins 2 and 3 (UCP2 &
 RT 3) and their localization to chromosome 9p by somatic cell hybrids";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Large white X Pietrain; TISSUE=Skeletal muscle;
 RA Damon M., Vincent A., Herpin P.;
 RT "First evidence of uncoupling protein (UCP) gene expression in piglet
 RT skeletal muscle";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS. THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).

```

CC CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC CC -!- SIMILARITY: Contains 3 Solcar repeats.
CC CC -----
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CC CC or send an email to license@sib-sib.ch).
CC CC -----
DR DR EMBL: AF095744; AAC08911.1; --
DR DR EMBL: AF128837; AAC33396.1; --
DR DR InterPro: IPR002067; Mit_carrier.
DR DR InterPro: IPR002030; Mit_uncoupling.
DR DR Pfam: PF00153; mito_carr; 3_
DR DR PRINTS: PR00926; MITOCARRIER.
DR DR PRINTS: PR00784; MTUNCOUPLING.
DR DR PROSITE: PS00920; SOLCAR; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 74 96 2 (POTENTIAL).
FT TRANSMEM 117 133 3 (POTENTIAL).
FT TRANSMEM 180 196 4 (POTENTIAL).
FT TRANSMEM 214 233 5 (POTENTIAL).
FT TRANSMEM 268 290 6 (POTENTIAL).
FT REPEAT 11 102 SOLCAR 1.
FT REPEAT 111 202 SOLCAR 2.
FT REPEAT 211 296 SOLCAR 3.
FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY
FT SIMILARITY).
FT CONFLICT 7 8 PE -> SD (IN REF. 2).
FT CONFLICT 13 13 T -> M (IN REF. 2).
FT CONFLICT 17 17 L -> F (IN REF. 2).
FT CONFLICT 49 49 A -> AVQT (IN REF. 2).
FT CONFLICT 150 150 R -> G (IN REF. 2).
SQ SEQUENCE 308 AA; 33772 MW; FDF1F2BC28FDE997 CRC64;

Query Match 28.4%; Score 480.5; DB 1; Length 308;
Best Local Similarity 34.5%; Pred. No. 3.5e-32;
Matches 108; Conservative 64; Mismatches 114; Indels 27; Gaps 6;

QY 20 ASKFLSGCAATVAELATFFLDLTKTQLQMGAAALRGDGAESAPYRGVMVLTALGII 79
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
14 AVKLGGAGTAACFADLLTFELDTAKVRLQIQENQAR-----SAQYRGVLGTLTMV 66
QY 80 EEEGFLKMGQVTPAIRVHVYGGRMVTVEHLREVVFGSKSEDEHYPLWKSIVGGMAGV 139
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
67 RNEGPRSPYNGVLVAGLQROQSFASIRIGLYDSVKQLYTPKGS-D-HGSITTRILAGCTGA 125
QY 140 IQGFLANPTDLVKVQMQME---GKRLEGKPLFRGVHFAFILAEGGIRGLWAGVVPN 196
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
126 MAVTCQPTDVVKRFPQASIHAGRSNR-----KYSGMTDAYRTAREEGVRLGWLKGLPN 181
QY 197 IQRAALVNMGDLTATYDVTHYLVNLTPLDNIHTHGLSSLCGLVASILGTPTADVTKSRI 256
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
182 ITRNAIVNCAEMTYDVIVKEKLDYHLLTDLNLFCHFSVAGFCATVVASPVDVVKTRY 241
QY 257 MNOPRKQKRGLLYKSTDCILQAVQGEPMISYKGLFPSWLRTWPMVFWLTYPKIR- 315
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
242 MNSFPQG-----YQNPLDCLMKWVTQEGTAFYKGTFTPSFLRLGSLVNNVWFVSYSQLR 295
QY 316 -----EMSGVSVPF 323
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
296 ALMKVQMLRESPP 308

RESULT 6
UCP3_HUMAN
ID UCP3_HUMAN STANDARD; PRT; 312 AA.
AC P55916; O60475; Q96HL3;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3 OR SLC25A9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97324095; PubMed=9180264;
RA Boss O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J.,
RA Rossier C., Muzzin P., Giacobino J.-P.;
RT "Uncoupling protein-3: a new member of the mitochondrial carrier
RT family with tissue-specific expression.";
RL FEBS Lett. 408:39-42(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS UCP3L AND UCP3S).
RX MEDLINE=97467322; PubMed=9325252;
RA Solanes G., Vidal-Puig A., Grujic D., Flier J.S., Lowell B.B.;
RT "The human uncoupling protein-3 gene. Genomic structure, chromosomal
RT localization, and genetic basis for short and long form
RT transcripts.";
RL J. Biol. Chem. 272:25433-25436(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97450925; PubMed=9305858;
RA Gong D.-W., He Y., Karas M., Reitman M.;
RT "Uncoupling protein-3 is a mediator of thermogenesis regulated by
RT thyroid hormone, beta3-adrenergic agonists, and leptin.";
RL J. Biol. Chem. 272:24129-24132(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98158426; PubMed=9498661;
RA Uthammer S.M., Dalgaard L.T., Soerensen T.I.A., Tybjaerg-Hansen A.,
RA Erwald S.A., Andersen T., Clausen J.O., Pedersen O.;
RT "Organisation of the coding exons and mutational screening of the
RT uncoupling protein 3 gene in subjects with juvenile-onset obesity.";
RL Diabetologia 41:241-244(1998).
RN [5]
RP SEQUENCE FROM N.A.
RX PubMed=10958796;
RA Esterbauer H., Oberkofler H., Kremler F., Strosberg A.D., Patsch W.;
RT "The uncoupling protein-3 gene is transcribed from tissue-specific
RT promoters in humans but not in rodents.";
RL J. Biol. Chem. 275:36394-36399(2000).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udutin T.B., Toshiyuki S., Carninci P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP VARIANT OBESITY ILE-102.

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RX MEDLINE=98443224; PubMed=9769326;
 RA Argyropoulos G., Brown A.M., Willi S.M., He Y., Reitman M.,
 RA Gervao S.M., Spruill I., Garvey W.T.;
 RT "Effects of mutations in the human uncoupling protein 3 gene on the
 RT respiratory quotient and fat oxidation in severe obesity and type 2
 RT diabetes.";
 RL J. Clin. Invest. 102:1345-1351(1998).
 RN [8].
 RP VARIANT OBESITY TRP-70.
 RA Brown A.M., Willi S.M., Argyropoulos G., Garvey W.T.;
 RT "A novel missense mutation, R70W, in the human uncoupling protein 3
 RT gene in a family with type 2 diabetes.";
 RL Hum. Mutat. 13:506-506(1999).
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- Event=Alternative splicing; Named isoforms=3;
 CC Name=UCP3L;
 CC IsoId=P55916-1; Sequence=Displayed;
 CC Name=UCP3S;
 CC IsoId=P55916-2; Sequence=VSP_003271;
 CC Name=3;
 CC IsoId=P55916-3; Sequence=VSP_003270;
 CC -1- TISSUE SPECIFICITY: Only in skeletal muscle and heart. Is more
 CC expressed in glycolytic than in oxidative skeletal muscles.
 CC -1- DISEASE: Defects in UCP3 could be involved in severe obesity
 CC [MIM:601665].
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
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 DR EMBL; U84763; AAC51367.1; -;
 DR EMBL; U82818; AAC51356.1; -;
 DR EMBL; AF001787; AAC51369.1; -;
 DR EMBL; AF011449; AAC51767.1; -;
 DR EMBL; AF012202; AAC51785.1; ALT INIT.
 DR EMBL; AF012197; AAC51785.1; JOINED.
 DR EMBL; AF012198; AAC51785.1; JOINED.
 DR EMBL; AF012199; AAC51785.1; JOINED.
 DR EMBL; AF012200; AAC51785.1; JOINED.
 DR EMBL; AF012201; AAC51785.1; JOINED.
 DR EMBL; AF026958; AAC18822.1; -;
 DR EMBL; AF026956; AAC18822.1; JOINED.
 DR EMBL; AF026957; AAC18822.1; JOINED.
 DR EMBL; AF050113; AAC02284.1; -;
 DR EMBL; BC008392; AA008392.1; -;
 DR PIR; JC5522; JC5522.
 DR Genew; HGNC:12519; UCP3.
 DR MIM; 602044; -;
 DR MIM; 601665; -;
 DR GO; GO:0005743; C:mitochondrial inner membrane; TAS.
 DR GO; GO:0005739; C:mitochondrion; TAS.
 DR GO; GO:0005739; F:transporter activity; TAS.
 DR GO; GO:0005215; F:uncoupling protein activity; TAS.
 DR GO; GO:0015302; F:lipid metabolism; TAS.
 DR GO; GO:0006629; P:lipid metabolism; TAS.
 DR GO; GO:0015992; P:proton transport; TAS.
 DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.

DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PRINTS; PRO0784; MTUNCOUPLING.
 DR PROSITE; PS00920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Alternative splicing; Disease mutation; Diabetes mellitus; Obesity.
 FT TRANSMEM 11 32
 FT TRANSMEM 77 99
 FT TRANSMEM 120 136
 FT TRANSMEM 184 200
 FT TRANSMEM 218 237
 FT TRANSMEM 272 294
 FT REPEAT 11 105
 FT REPEAT 114 206
 FT REPEAT 215 300
 FT DOMAIN 279 301
 FT VARSPIC 114 216
 FT VARSPIC 276 312
 FT VARIANT 70 70
 FT VARIANT 102 102
 FT CONFLICT 193 194
 FT SEQUENCE 312 AA; 34216 MW; D0E04A8DB352B17C CRC64;
 SQ
 Query Match 28.1%; Score 475.5; DB 1; Length 312;
 Best Local Similarity 35.8%; Pred. No. 9.2e-32;
 Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;
 QY 20 ASKFLSLGCAATVAELATPDLTKRLQWQGE---AALARLGDGARESAFYRGWVRTAL 76
 DB 14 AVKFLGAGTAACFADLVTPDLTKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66
 QY 77 GIIEEGFLKLQGVTPAIYRHVVYSGGRMVYEHLEHREVFVGKSEDEHYPLMKSVIGMM 136
 DB 67 TWVTEGPCSPYNGLVAGLQRMSPASIRIGLYDSVKQVYTPKGAD-NSSLTRILAGCT 125
 QY 137 AGVIGOFPLANTDLVKVQWQME---GKRKLEKGLFRFRGVHAFKILAEGGIRGLWAGW 193
 DB 126 TGAAMVTCQPTDWWKVRFOASIHGLSPSRDRK---YSGTMDAYRTIAREEGVRGLWKG 182
 QY 194 VPMIOAALVNMGDLTYDTVKHYLVNTPLEDNIMTHGLSLCSGLVASILGTTPADVIK 253
 DB 183 LPNIMNAIVNCAEVVYDILKEKLDYHLLTDNFPCHFVSAGAGCATVVASPVDVVK 242
 QY 254 SRIMNQPRDKQGRGLLYKSTDCILQAVOGEGPMSLYKGLFSLWLRMTWPMVFWLTYEK 313
 DB 243 TRYNSPPGQ-----YFSPFLDCMIKWVAQEGPTAFYKGTFTSFLRLGSLNVMVFTYEQ 296
 QY 314 IR-----EMSGVSPF 323
 DB 297 LKRALMKVQMLRESPP 312
 RESULT 7
 UCP3_CANPA STANDARD; PRT; 311 AA.
 AC Q9N219; Q9TTS9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 3 (UCP 3).
 GN UCP3.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.

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RA Iishioka K.;
RT "Cloning of canine UCP families.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 14-146 FROM N.A.
RA Thompson G.M., Kelly L.J., Candelore M.R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
CC ENERGY BALANCE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -!- SIMILARITY: Contains 3 Solcar repeats.
CC
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CC
CC EMBL: AB022020; BAA90458.1; -
CC EMBL: AF201378; AAF08310.1; -
CC InterPro: IPR002030; Mit_uncoupling.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carr; 3.
CC DR PRINTS: PR00784; MTUNCOUPLING.
CC DR PROSITE: PS50920; SOLCAR; 3.
KW Mitochondrion; Inner membrane; Repeat: Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 77 99
FT TRANSMEM 120 136
FT TRANSMEM 183 199
FT TRANSMEM 217 236
FT TRANSMEM 271 293
FT REPEAT 11 105
FT REPEAT 114 205
FT REPEAT 214 299
FT DOMAIN 278 300
FT
FT CONFLICT 14 14 A -> G (IN REF. 2).
FT SEQUENCE 311 AA; 34137 MW; A719FB8D66637502 CRC64;

Query Match 28.0%; Score 474; DB 1; Length 311;
Best Local Similarity 34.8%; Pred. No. 1.2e-31;
Matches 109; Conservative 59; Mismatches 121; Indels 24; Gaps 6;

QY 20 ASKFLSGCAATVAELATPPLDTKTRLQWQGAALRLGDGAREAPYRGWRTALGII 79
DB 14 AVKFLGAGTAACPADLLTTPDLAKVRLQIQGENQATQ-----AARRIQYRGVLGTLTWV 69
QY 80 EEEGLKMQGVTPAIVRYHVYSGGRMTVYHLEHREVVFCKSEDEHYPLMKSVIGGMAGV 139
DB 70 RTGGPSYNGLVAGIQRQMSFASIRIGLYDSVQFYTPKGS-D-HSITRILAGCTTGA 128
QY 140 IQGFLANPDLVQVQME---GKRKLEGLKPLFRGVHFAKILAEGGIRGLWAGVVPN 196
DB 129 MAVSCAQPTDVVKVRQASHTLG-----AGSNRKYSGTMDAYRTIAREEGVRLGWLKGTLPN 184
QY 197 IQRAALVNGDLTYTIVKHYLVNTPLEDNIMTHGLSSLCGSLVASILGTTPADVTKSRI 256
DB 185 ITRNAIVNCAEMVTDIIEKLDYHLLTDNFPFCHLISAFAGFCATVWASPDVVKTRY 244
QY 257 MNQPRDKQGRGLLYKSSDCLIOAVQEGPMSLYKGLPSLWLRMTWSMVFWLTYEKIR- 315
DB 245 MNSPPCQ-----YCSPLDCMLKQKVTQBGPTAFYKGTFTSFLRLGTVNMVFMVTEYQLKR 298
QY 316 -----EMSGVSPF 323

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Db 299 ALMKVQMLRESPF 311
RESULT 8
UCP3_MOUSE
ID UCP3_MOUSE STANDARD; PRT; 308 AA.
AC PS6501; O89293;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sanchis D., Fleury C., Bouillaud F., Ricquier D.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Embryo;
RX MEDLINE=98332721; PubMed=9666083;
RA Yoshitomi H., Yamazaki K., Tanaka I.;
RT "Cloning of mouse uncoupling protein 3 cDNA and 5'-flanking region,
RL and its genetic map.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Skeletal muscle;
RA Grujic D., Zhan C.-Y., Sleiker L.J., Lowell B.B.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skeletal muscle;
RA Son C., Hoboda K., Matsuda J., Nakao K.;
RT "Cloning of mouse UCP3 cDNA.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99167332; PubMed=10066417;
RA Gong D.W., He Y., Reitman M.L.;
RT "Genomic organization and regulation by dietary fat of the uncoupling
RL protein 3 and 2 genes.";
RN [6]
RP Biochem. Biophys. Res. Commun. 256:27-32(1999).
RC SEQUENCE OF 84-180 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;
RX MEDLINE=98262957; PubMed=9600108;
RA Shimokawa T., Kato M., Ezaki O., Hashimoto S.;
RT "Transcriptional regulation of muscle-specific genes during myoblast
RL differentiation.";
RN [7]
RP Biochem. Biophys. Res. Commun. 246:287-292(1998).
RP SEQUENCE OF 162-252 FROM N.A.
RA Yan X., Ramsay T.G.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
CC ENERGY BALANCE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -!- SIMILARITY: Contains 3 Solcar repeats.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB022020; BAA90458.1; -
CC EMBL: AF201378; AAF08310.1; -
CC InterPro: IPR002030; Mit_uncoupling.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carr; 3.
CC DR PRINTS: PR00784; MTUNCOUPLING.
CC DR PROSITE: PS50920; SOLCAR; 3.
KW Mitochondrion; Inner membrane; Repeat: Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 77 99
FT TRANSMEM 120 136
FT TRANSMEM 183 199
FT TRANSMEM 217 236
FT TRANSMEM 271 293
FT REPEAT 11 105
FT REPEAT 114 205
FT REPEAT 214 299
FT DOMAIN 278 300
FT
FT CONFLICT 14 14 A -> G (IN REF. 2).
FT SEQUENCE 311 AA; 34137 MW; A719FB8D66637502 CRC64;

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predominant expression in the heart, lung and spleen.
 -!- SIMILARITY: Belongs to the mitochondrial carrier family.
 -!- SIMILARITY: Contains 3 Solcar repeats.

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 EMBL; AF039033; AAC98733.1; -
 EMBL; AB006613; BAA23383.1; -
 EMBL; AB010743; BAA25698.1; -
 EMBL; AB005143; BAA28832.1; -
 InterPro; IPR002030; Mit_uncoupling.
 InterPro; IPR001993; Mitoch_carrier.
 Pfam; PF00153; mito_carr; 3.
 PRINTS; PR00784; MTUNCOUPLING.
 PROSITE; PS0920; SOLCAR; 3.

Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 TRANSMEM 11 32 1 (POTENTIAL).
 TRANSMEM 78 100 2 (POTENTIAL).
 TRANSMEM 120 136 3 (POTENTIAL).
 TRANSMEM 181 197 4 (POTENTIAL).
 TRANSMEM 215 234 5 (POTENTIAL).
 TRANSMEM 269 291 6 (POTENTIAL).
 REPEAT 11 106 SOLCAR 1.
 REPEAT 114 203 SOLCAR 2.
 REPEAT 212 297 SOLCAR 3.
 DOMAIN 276 298

CONFLICT 9 9 V -> L (IN REF. 4).
 CONFLICT 268 268 A -> T (IN REF. 3).
 CONFLICT 309 AA; 33376 MW; 3297935CF997AA0E CRC64;

Query Match 28.0%; Score 473.5; DB 1; Length 309;
 Best Local Similarity 35.0%; Pred. No. 1.3e-31;
 Matches 105; Conservative 65; Mismatches 113; Indels 17; Gaps 6;

18 PRAS-KFLISGCAATVAELATFPLDITKRLQMGEEA-ALARGDGAHAPYRGWRTA 75
 11 PTATVKFLGAGTAACIADLTITFPLDTAKRLQIGESQGLAR----TAASAQYRGVLGTI 66
 76 LGITEEGFLKMGQVTPAIYRHVYVGGRMVTVYHLREVVGKSEDEHYPLWKSIVGGM 135
 67 LTMVTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ---FYTKGSEHAGISRLLAGS 124
 136 MAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRFRGVHFAKILAEGGIRGLWAGWVP 195
 125 TTGALAVAVAQPTDVVKRFQAQAR---AGGRRYQSTVEAYKTIAREEGIRGLWKGTSR 181
 196 NIQRAALVNMGDLTITYDTVKHYLVNTPLEDNIMTHGLSLCSGLVASILGTPADVIKSR 255
 182 NVARNAINVNCALVTYDLIKDALLKANLMTDDLPCHFTSAFGAGCTCTVIASPDVVVKTR 241
 256 IMNQPRDKQGRGLLYKSSDCLIOAVQGEFMSLYKGLFPLSWLRMTFWSVFWLTYSKIR 315
 242 YMNSALGQ-----YHSAGHCALTMRLKRGFPAYKGFMPESFLRLGSMVNVFVTEYQLK 295

RESULT 11
 UCP2_CANFA STANDARD; PRT; 309 AA.
 AC Q9N2J1; Q9TTT0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 2 (UCP 2).
 GN UCP2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 [1]
 RN SEQUENCE FROM N.A.
 RA Ishioka K.;
 RT "Cloning of canine UCP families.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE OF 4-197 FROM N.A.
 RA Thompson G.M., Kelly L.J., Candelore M.R.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: UCP are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. As a result, energy is dissipated in the form of heat (By similarity).
 CC -!- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -!- SIMILARITY: Contains 3 Solcar repeats.

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 EMBL; AB020887; BAA90457.1; -
 EMBL; AF201377; AAF08309.1; -
 InterPro; IPR002030; Mit_uncoupling.
 InterPro; IPR001993; Mitoch_carrier.
 Pfam; PF00153; mito_carr; 3.
 PRINTS; PR00784; MTUNCOUPLING.
 PROSITE; PS0920; SOLCAR; 3.

Mitochondrion; Transmembrane; Transport; Repeat.
 TRANSMEM 11 32 1 (POTENTIAL).
 TRANSMEM 78 100 2 (POTENTIAL).
 TRANSMEM 120 136 3 (POTENTIAL).
 TRANSMEM 181 197 4 (POTENTIAL).
 TRANSMEM 215 234 5 (POTENTIAL).
 TRANSMEM 269 291 6 (POTENTIAL).
 REPEAT 11 106 SOLCAR 1.
 REPEAT 114 203 SOLCAR 2.
 REPEAT 212 297 SOLCAR 3.
 DOMAIN 276 298

CONFLICT 64 64 PURINE NUCLEOTIDE BINDING (BY
 CONFLICT C -> G (IN REF. 2).
 CONFLICT 309 AA; 33270 MW; D9860F0EA8B870BF CRC64;

Query Match 28.0%; Score 472.5; DB 1; Length 309;
 Best Local Similarity 35.0%; Pred. No. 1.6e-31;
 Matches 105; Conservative 63; Mismatches 115; Indels 17; Gaps 6;

18 PRAS-KFLISGCAATVAELATFPLDITKRLQMGEEAALARGD-GARESAPYRGWRTA 75
 11 PTATVKFLGAGTAACIADLTITFPLDTAKRLQIGEE---RQGPVRAAASQYRGVLCTI 66
 76 LGITEEGFLKMGQVTPAIYRHVYVGGRMVTVYHLREVVGKSEDEHYPLWKSIVGGM 135
 67 LTMVTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ---FYTKGSEHAGISRLLAGS 124
 136 MAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLRFRGVHFAKILAEGGIRGLWAGWVP 195
 125 TTGALAVAVAQPTDVVKRFQAQAR---AGGRRYQSTVDAYKTIAREEGIRGLWKGTSR 181
 196 NIQRAALVNMGDLTITYDTVKHYLVNTPLEDNIMTHGLSLCSGLVASILGTPADVIKSR 255
 182 NVARNAINVNCALVTYDLIKDALLKANLMTDDLPCHFTSAFGAGCTCTVIASPDVVVKTR 241
 256 IMNQPRDKQGRGLLYKSSDCLIOAVQGEFMSLYKGLFPLSWLRMTFWSVFWLTYSKIR 315


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DE Mitochondrial uncoupling protein 2 (UCP 2).
GN UCP2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Werner P., Nowaczyk K., Neuenchwander S., Strazinger G.;
RT Characterization of the porcine uncoupling proteins 2 and 3 (UCP2 &
RT 3) and their localization to chromosome 9p by somatic cell hybrids.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 114-211 FROM N.A.
RA Fang M.-Y., Zhao X.-B., Li N.;
RT "Exon 3, intron 3 and exon 4 sequencing of porcine uncoupling protein
RT 2 gene.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: UCP are mitochondrial transporter proteins that create
CC proton leaks across the inner mitochondrial membrane, thus a
CC uncoupling oxidative phosphorylation from ATP synthesis. As a
CC result, energy is dissipated in the form of heat (By similarity).
CC -!- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -!- SIMILARITY: Contains 3 Solcar repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC
CC EMBL; AF036757; AAD05201.1; -.
CC EMBL; AF332003; AAG45440.1; -.
CC InterPro; IPR002030; Mit_uncoupling.
CC InterPro; IPR001993; Mitoch_carrier.
CC Pfam; PF00153; mito_carr; 3.
CC PRINTS; PR00784; MTUNCOUPLING.
CC PROSITE; PS00920; SOLCAR; 3.
CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
CC TRANSMEM 11 32 1 (POTENTIAL).
CC TRANSMEM 78 100 2 (POTENTIAL).
CC TRANSMEM 120 136 3 (POTENTIAL).
CC TRANSMEM 181 197 4 (POTENTIAL).
CC TRANSMEM 215 234 5 (POTENTIAL).
CC TRANSMEM 269 291 6 (POTENTIAL).
CC REPEAT 11 106 SOLCAR 1.
CC REPEAT 114 203 SOLCAR 2.
CC REPEAT 212 297 SOLCAR 3.
CC DOMAIN 276 298
CC
CC CONFLICT 115 115 G -> S (IN REF. 2).
CC CONFLICT 208 208 D -> N (IN REF. 2).
CC SEQUENCE 309 AA; 33259 MW; 7A67D59946DA21BD CRC64;
CC
CC Query Match 28.0%; Score 472.5; DB 1; Length 309;
CC Best Local Similarity 35.3%; Pred.No. 1.6e-31;
CC Matches 106; Conservative 61; Mismatches 116; Indels 17; Gaps 6;
CC
CC 18 PRAS-KFLLSGCAATVAELATFPLDLTKFLQMGQEAALALRGD-CARBSAPYRGWVITA 75
CC 11 PTAIVFLGAGTACACADLTTFEDTAKVRLQIQE-----RRGPAASAQRGVIGTI 66
CC
CC 76 LGIIEEGFLKLQGVTPAIYRHVYVSGRMVYIEHLREVVFQKSDDEHYPLWKSIVIGM 135
CC 67 LTVWRNEGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKH--FYTKGSEHAGIGSRLLAGS 124
CC
CC 136 MAGVIQGFANPTDLVQVQMQMEGKRLKGLKPLRFRGVHFAFAKILAEGRGLMAGWVP 195

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Db 125 TTGALAVANAQPTDVVKVRFAQAR---AGGRRYRSTVDYAKTIAREEGLRLWKGTS 181
Qy 196 NIQRAALVNMGDLTYYTVKHYLVLTNPLEDNIMTHGLSLCSGLVASILGTTPADVIKSR 255
Db 182 NVARNALVNCALVTVYDLIKDTLLKADLMTDLPCHFTSAFGAGFCTTVIASPDVVVKTR 241
Qy 256 IMNQPRDKQGRGLLYKSSDCLIQAVQEGFMSLYKGLPLPSMLRMTWPSVFWLTVEKIR 315
Db 242 YMNSAPCQ-----YSSAGHCALMTLQKGFAPFYKGFPSFLRLGLGWNVVMFVTEQLK 295

RESULT 14
UCP3_RAT STANDARD; PRT; 308 AA.
AC PS6439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RX MEDLINE=98074937; PubMed=9414126;
RA Matsuda J., Hosoda K., Itoh K., Son C., Doi K., Tanaka T.,
RA Fukunaga Y., Inoue G., Nishimura H., Yoshimasa Y., Yamori Y.,
RA Nakao K.;
RT "Cloning of rat uncoupling protein-3 and uncoupling protein-2 cDNAs:
RT their gene expression in rats fed high-fat diet.";
RL FEBS Lett. 418:200-204(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Skeletal muscle;
RX MEDLINE=98165302; PubMed=9506477;
RA Boss O., Samec S., Desplanches D., Mayet M.-H., Seydoux J., Muzzin P.,
RA Giacobino J.-P.;
RT "Effect of endurance training on mRNA expression of uncoupling
RT proteins 1, 2, and 3 in the rat.";
RL FASEB J. 12:335-339(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RX MEDLINE=98400868; PubMed=9725803;
RA Lin B.-Z., Coughlin S., Pilch P.F.;
RT "Bidirectional regulation of uncoupling protein-3 and GLUT-4 mRNA in
RT skeletal muscle by cold";
RL Am. J. Physiol. 275:E386-E391(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RA Solanes G., Valet P., Lowell B.B.;
RT "Lipopolysaccharide treatment increases thermogenesis and induces
RT uncoupling protein-3 gene expression in skeletal muscle.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
CC ENERGY BALANCE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral
CC inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -!- SIMILARITY: Contains 3 Solcar repeats.
CC
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RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Hitomi Y., Moriya S., Matsushita K., Tanaka H.;
 RT "Molecular cloning of mouse UCP4 cDNA."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AK014394; BAB29320.1; -;
 DR EMBL; AK043831; BAC31670.1; -;
 DR EMBL; AB106930; BAC66453.1; -;
 DR MGD; MGI:1921261; 3632410G24Rik.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS002030; Mit uncoupling.
 DR InterPro; IPR002030; Mit uncoupling.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 322 AA; 35798 MW; 9C8A413DD28E1B8A CRC64;
 Query Match 95.9%; Score 1621; DB 11; Length 322;
 Best Local Similarity 96.2%; Pred. No. 5.8e-130;
 Matches 306; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 6 EEEELLPRTQWRPRASKFLSGCAATVAELATPDLTKTRLOMQGAALRLGDGARES 65
 DB 5 EEEKLLPRTQWRPRTSKFLSGCAATVAELATPDLTKTRLOMQGAALRLGDGAVDS 64
 QY 66 APYRGWRTALGIIEEGFLKMQGVTPAIYRHVVYSGGRMTVEHLREVVFSGSDEHY 125
 DB 65 APYRGWRTALGIIVQEGFLKMQGVTPAIYRHVVYSGGRMTVEHLREVVFSGSKDHY 124
 QY 126 PLKWSVIGGMAGVIGQFLANPTDLVKVQMGEGKRLKPLRFRGVHAFKILAEAG 185
 DB 125 PLKWSVIGGMAGVIGQFLANPTDLVKVQMGEGKRLKPLRFRGVHAFKILAEAG 184
 QY 186 IRLGAGWPNIOQAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGLVASIL 245
 DB 185 IRLGAGWPNIOQAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGLVASIL 244
 QY 246 GTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFGMSLYKGFPSWLRTPWSM 305
 DB 245 GTPADVIKSRIMNQPRDKQGRGLLYKSSADCLIQAVQGEFGFLSYKGFPSWLRTPWSM 304
 QY 306 VFVLTVEKIREMSGVSPP 323
 DB 305 VFVLTVEKIREMSGVSPP 322
 RESULT 2
 Q9EPH7 PRELIMINARY; PRT; 322 AA.
 ID Q9EPH7
 AC Q9EPH7
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Uncoupling protein UCP-4, isoform a.
 GN UCP-4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Brain;
 RA Alberati-Giani D., Gatti S., Rial E., Danel F., Hauser N.,
 RA Bubendorff C., Bartfal T.;
 RT "Three different isoforms of UCP-4 are expressed in rat preoptic
 RT anterior hypothalamus.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AJ300162; CAC20898.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 322 AA; 35837 MW; 454580DCA80A9F90 CRC64;
 Query Match 94.9%; Score 1603.5; DB 11; Length 322;
 Best Local Similarity 94.1%; Pred. No. 1.8e-128;
 Matches 304; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MSVPEEEERLLPRTQWRPRASKFLSGCAATVAELATPDLTKTRLOMQGAALRLGD 60
 DB 1 MPPEEES-LQPLTQWRPRTSKFLSGCAATVAELATPDLTKTRLOMQGAALRLGD 59
 QY 61 GAREAPYRGWRTALGIIEEGFLKMQGVTPAIYRHVVYSGGRMTVEHLREVVFSGS 120
 DB 60 GAREAPYRGWRTALGIIVQEGFLKMQGVTPAIYRHVVYSGGRMTVEHLREVVFSGS 119
 QY 121 EDEHPLKWSVIGGMAGVIGQFLANPTDLVKVQMGEGKRLKPLRFRGVHAFKILAE 180
 DB 120 EDEHPLKWSVIGGMAGVIGQFLANPTDLVKVQMGEGKRLKPLRFRGVHAFKILAE 179
 QY 181 LAEGGIRGLWAGWPNIOQAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGL 240
 DB 180 LAEGGIRGLWAGWPNIOQAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGL 239
 QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFGMSLYKGFPSWLRM 300
 DB 240 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFGFLSYKGFPSWLRM 299
 QY 301 TPWSMVFWLTVEKIREMSGVSPP 323
 DB 300 TPWSMVFWLTVEKIREMSGVSPP 322
 RESULT 3
 Q9EPH6 PRELIMINARY; PRT; 344 AA.
 ID Q9EPH6
 AC Q9EPH6
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Uncoupling protein UCP-4, isoform b.
 GN UCP-4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Brain;
 RA Alberati-Giani D., Gatti S., Rial E., Danel F., Hauser N.,
 RA Bubendorff C., Bartfal T.;

"Three different isoforms of UCP-4 are expressed in rat preoptic anterior hypothalamus.";
 Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AJ300163; CAC20899.1; -;
 GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO: GO:0005739; C:mitochondrion; IEA.

DR GO: GO:0005488; F:binding; IEA.

DR GO: GO:0006839; P:mitochondrial transport; IEA.

DR GO: GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch_carrier.

DR InterPro; IPR002030; Mit uncoupling.

DR Pfam; PF00153; mito carr; 3.

DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH_CARRIER; 2.

KW Membrane; Transmembrane; Transport.

SQ SEQUENCE 344 AA; 38114 MW; 600ACBSF366BADAA CRC64;

Query Match 87.6%; Score 1480.5; DB 11; Length 344;
 Best Local Similarity 94.3%; Pred. No. 6.2e-118;
 Matches 283; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 MSVPSEERLLPTQWRPASKFLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 60

DB 1 MPPEEES-LQPLTQWRPRTSKFLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 59

QY 61 GAREAPYRGWMTALGIIEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 120

DB 60 GAMESAPYRGWMTALGIQVEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 119

QY 121 EDEHYPLWKSIVIGMAGVIGQFLANPTDLVKVQMQMEGKRKLEKPLRFRGVHHAFAKI 180

DB 120 EDEHYPLWKSIVIGMAGVIGQFLANPTDLVKVQMQMEGKRKLEKPLRFRGVHHAFAKI 179

QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDTVKHYLVNTPLENIMTHGLSSLCGSL 240

DB 180 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDTVKHYLVNTPLENIMTHGLSSLCGSL 239

QY 241 VASILGTADVIKSRIMNPRDKQGRGLLYKSTDCVIAQVQEGFSLYKGLFPLSLRM 300

DB 240 VASILGTADVIKSRIMNPRDKQGRGLLYKSTDCVIAQVQEGFSLYKGLFPLSLRM 299

QY 121 EDEHYPLWKSIVIGMAGVIGQFLANPTDLVKVQMQMEGKRKLEKPLRFRGVHHAFAKI 180

DB 120 EDEHYPLWKSIVIGMAGVIGQFLANPTDLVKVQMQMEGKRKLEKPLRFRGVHHAFAKI 179

QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDTVKHYLVNTPLENIMTHGLSSLCGSL 240

DB 180 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDTVKHYLVNTPLENIMTHGLSSLCGSL 239

QY 241 VASILGTADVIKSRIMNPRDKQGRGLLYKSTDCVIAQVQEGFSLYKGLFPLSLRM 300

DB 240 VASILGTADVIKSRIMNPRDKQGRGLLYKSTDCVIAQVQEGFSLYKGLFPLSLRM 299

RESULT 4
 Q9EPH5 PRELIMINARY; PRT; 365 AA.

AC Q9EPH5; STRAIN=C57BL/6J; TISSUE=Stomach;

DT 01-MAR-2001 (T-EMBLrel. 16, Created)

DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Uncoupling protein UCP-4, isoform C.

GN UCP-4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague Dawley; TISSUE=Brain;

RC Alberati-Giani D., Gatti S., Rial E., Danel F., Hauser N.,

RA Bubendorff C., Bartfai T.

RT "Three different isoforms of UCP-4 are expressed in rat preoptic

hypothalamus.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AJ300164; CAC20900.1; -;

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO: GO:0005739; C:mitochondrion; IEA.

DR GO: GO:0005488; F:binding; IEA.

DR GO: GO:0006839; P:mitochondrial transport; IEA.

DR GO: GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR Pfam; PF00153; mito carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 365 AA; 41144 MW; 477B3898BE1F7525 CRC64;

Query Match 87.6%; Score 1480.5; DB 11; Length 365;
 Best Local Similarity 94.3%; Pred. No. 6.7e-118;
 Matches 283; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 MSVPSEERLLPTQWRPASKFLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 60

DB 1 MPPEEES-LQPLTQWRPRTSKFLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 59

QY 61 GAREAPYRGWMTALGIIEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 120

DB 60 GAMESAPYRGWMTALGIQVEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 119

QY 121 EDEHYPLWKSIVIGMAGVIGQFLANPTDLVKVQMQMEGKRKLEKPLRFRGVHHAFAKI 180

DB 120 EDEHYPLWKSIVIGMAGVIGQFLANPTDLVKVQMQMEGKRKLEKPLRFRGVHHAFAKI 179

QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDTVKHYLVNTPLENIMTHGLSSLCGSL 240

DB 180 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDTVKHYLVNTPLENIMTHGLSSLCGSL 239

QY 241 VASILGTADVIKSRIMNPRDKQGRGLLYKSTDCVIAQVQEGFSLYKGLFPLSLRM 300

DB 240 VASILGTADVIKSRIMNPRDKQGRGLLYKSTDCVIAQVQEGFSLYKGLFPLSLRM 299

RESULT 5
 Q9CX10 PRELIMINARY; PRT; 283 AA.

ID Q9CX10; STRAIN=C57BL/6J; TISSUE=Stomach;

DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE D530043E16RIK protein.

GN 3632410G24RIK OR D530043E16RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Stomach;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AK021314; BAB32369.1; -;

DR MGD; MGI:1921261; 3632410G24RIK.

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DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR GO: GO:0005488; P:binding; IEA.
DR GO: GO:0006839; P:mitochondrial transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 283 AA; 31122 MW; 8645127817A51864 CRC64;

Query Match 78.0%; Score 1319; DB 11; Length 283;
Best Local Similarity 95.1%; Pred. No. 2.9e-104;
Matches 250; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 6 EEEELLPLOTQWRPRASKFLSGCAATVAELATFPDLTKTLQMGGAALRLGDGARES 65
Db 5 EEEKLLPLOTQWRPRASKFLSGCAATVAELATFPDLTKTLQMGGAALRLGDGAVDS 64

Qy 66 APYRGWVRTALGIIEEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDEHY 125
Db 65 APYRGWVRTALGIIVQEEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDKHY 124

Qy 126 PLWKSIVGGMAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHHAFAKILAEQG 185
Db 125 PLWKSIVGGMAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHHAFAKILAEQG 184

Qy 186 IRGLWAGWPNIQRAALVNMGLTDTYDVKHVYLVNTPLEDNIMTHGLSLCSGLVASIL 245
Db 185 IRGLWAGWPNIQRAALVNMGLTDTYDVKHVYLVNTPLEDNIMTHGLSLCSGLVASIL 244

Qy 246 GTPADVIKSRIMNPQDKQGRGL 268
Db 245 GTPADVIKSRIMNPQDKQGRSV 267

RESULT 6
Q8N518 PRELIMINARY; PRT; 245 AA.
AC Q8N518;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to uncoupling protein 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC033091; AAH33091.1; -
DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO: GO:0005488; P:binding; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 2.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 245 AA; 27237 MW; 4D1C41017B67DA68 CRC64;

Query Match 72.2%; Score 1221; DB 4; Length 245;
Best Local Similarity 99.6%; Pred. No. 5.4e-96;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSVPEEERLLPLOTQWRPRASKFLSGCAATVAELATFPDLTKTLQMGGAALRLGD 60
Db 1 MSVPEEERLLPLOTQWRPRASKFLSGCAATVAELATFPDLTKTLQMGGAALRLGD 60

GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0005743; C:mitochondrial inner membrane; IEA.
GO: GO:0005739; C:mitochondrion; IEA.
GO: GO:0005488; P:binding; IEA.
GO: GO:0006839; P:mitochondrial transport; IEA.
GO: GO:0006810; P:transport; IEA.
InterPro: IPR001993; Mitoch_carrier.
InterPro: IPR002030; Mit_uncoupling.
Pfam: PF00153; mito_carr; 3.
PRINTS: PR00784; MTUNCOUPLING.
PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 283 AA; 31122 MW; 8645127817A51864 CRC64;

Query Match 70.6%; Score 1192.5; DB 13; Length 315;
Best Local Similarity 69.5%; Pred. No. 2e-93;
Matches 214; Conservative 46; Mismatches 47; Indels 1; Gaps 1;

Qy 16 RWPRAKFLSGCAATVAELATFPDLTKTLQMGGAALRLGDGARESAPYRGWVRTA 75
Db 9 RWPRAKFLSGCAATVAELATFPDLTKTLQMGGAALRLGDGARESAPYRGWVRTA 67

Qy 76 LGIIEEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDEHYPLWKSIVGGM 135
Db 68 AGIVREEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDEHYPLWKSIVGGM 127

Qy 136 MAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHHAFAKILAEQGIKRLWAGWVP 195
Db 136 MAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHHAFAKILAEQGIKRLWAGWVP 195

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Db 128 ISGALGQFIASPTDLVKVQVQMEGRRLKGGPPRVGCVHYAFTKIVAQQGIRGLWAGWVP 187
QY 196 NIQRAALVNMGDLITTYDVVKHYLVNTPLENDIMTHGLSLCGLVASIILGTPADVIKSR 255
Db 188 NVQRAALVNLGDLMTYDVVKHFLRNTSIPDNSICHLSSICGLVNAATGTTADVVVKTR 247
QY 256 INQPRDKQGRGLLYKSSDCLIAVQGEFMSLYKGFPLSWLRMTWMSVFWLTVEKIR 315
Db 248 VMNQPRDSNGRGLLYNRNSTDCLVQSVRRGFFSLYKGFPLTFWFMAPSLSLTFWLTPEQLR 307
QY 316 EMSGVSPF 323
Db 308 RAMG1SSF 315

RESULT 8
Q9VX14 PRELIMINARY; PRT; 340 AA.
ID Q9VX14 AC Q9VX14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG6492 protein.
GN UCP4 OR CG6492.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Hoskins R.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Geibart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB003506; AAF48769.1; -

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DR FlyBase; FBgn0030872; Ucp4A.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006839; P:mitochondrial transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 340 AA; 37096 MW; E452932B7C1C46D1 CRC64;

Query Match 55.2%; Score 933; DB 5; Length 340;
Best Local Similarity 57.2%; Pred. No. 3.1e-71;
Matches 174; Conservative 56; Mismatches 70; Indels 4; Gaps 2;

QY 20 ASKFLSLGCAATVAELATPDLTKTRLOMQGAALRLGDGARESAAPYRGMYRTALGII 79
Db 41 ACTYIVSVVAASIAELATPDLTKTRLOMQGAASAG---KSNMQYKGMVATATGIA 97
QY 80 EEEGFLKMQGVTPALYRHYVYSGRMVYEHURVVFVGSDEHPLKWSVIGMMAGV 139
Db 98 REEGALKMQGVTPALYRHYVYSGVRYCSYDLMRK-EFTQNGTQALPVMKSAALCGVTAGA 156
QY 140 IGOFLANPTDLVKVQVQMEGRRLKGGPPRVGCVHYAFTKIVAQQGIRGLWAGWVPNIOR 199
Db 157 VAQWLASPADLVKVQVQMEGRRLKGGPPRVGCVHYAFTKIVAQQGIRGLWAGWVPNIOR 216
QY 200 AALVNMGDLITTYDVVKHYLVNTPLENDIMTHGLSLCGLVASIILGTPADVIKSRIMNQ 259
Db 217 AALVNLGDLITTYDVVKHFLRNTSIPDNSICHLSSICGLVNAATGTTADVVVKTRIMNQ 276
QY 260 PRDKQGRGLLYKSSDCLIAVQGEFMSLYKGFPLSWLRMTWMSVFWLTVEKIRMSG 319
Db 277 PTDENGRGLLYRGSVDCLRQTVSGEVALYKGFPLPCWIRMAPSLTFWLTPEQLRKWIG 336
QY 320 VSPF 323
Db 337 ASGY 340

RESULT 9
O01883 PRELIMINARY; PRT; 324 AA.
ID O01883 AC O01883;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN K07B1.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. the C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid K07B1.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the ENBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF003384; AAB54239.2; -
DR PIR; T15253; T15253.
DR WormPep; K07B1.3; CE28591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
DR Hypothetical protein; Membrane; Transmembrane; Transport.
KW SEQUENCE 334 AA; 36572 MW; DF48DB24C0F3A129 CRC64;

Query Match 47.0%; Score 793.5; DB 5; Length 324;
Best Local Similarity 48.2%; Pred. No. 2.3e-59;
Matches 151; Conservative 57; Mismatches 84; Indels 21; Gaps 2;

QY 20 ASKELSGCAATVAELATFPDLTKTQLWQGEAALRLGDAESAPYGMVKTALGII 79
DB 24 ATKYFSLCTAALVAETVYPLDIKTRLQI-----ARNKFTKGMVQVTVYDII 71
QY 80 EEEGFLKMOGVTPAIYRHHVYSGRMVTVYHLEHREVFGKSEDEHYPLWKSIVGGMAGV 139
DB 72 RREGAMALWTGAPATTHYYITGIRMGAYEQIRLITFNKEVSKFPLWKSMLCGAFSGL 131
QY 140 IGQFLANPTDLVKVQMQEGRKLEKGLRFRGVHHAFAKILAEGGIRGLWAGVWPNIOR 199
DB 132 IAQPAASPTDLVKVQMQEGLRLKQPLATYGTATDCFRSLYRTQGFGLWGMPCOR 191
QY 200 AALVNMGDLTYTVKHYLVNTPLEDNINTHGLSSLCGLVASILGTTPADVTKSRIMNQ 259
DB 192 AALLNADIATYSVSRKGLINDFELKDNWLTHAVASACAGLAAIYSLPSDVVVKTRMMDQ 251
QY 260 PRDKQGRGLLYKYST-----DCLIQAVOGEFMSLYKGFPLPSMLRTPMSVMFWLT 310
DB 252 IRHLEDAKMHKKNTHVDLYKGVVDCVIKIKNEGFSLYKGFPLPSVIRMAPSLTFWVS 311
QY 311 YEKIREMSGVSPF 323
DB 312 YEEIKRTGASSF 324

RESULT 10
Q9VMK0
ID Q9VMK0 PRELIMINARY; PRT; 337 AA.
AC Q9VMK0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG18340 protein.
GN UCP4B OR CG18340.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolehakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Goddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swierkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AS003612; AAF52314.1; -
DR FlyBase; FBgn0031758; Ucp4B.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:mitochondrial transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito car; 3.
DR PRINTS; PR00784; MTUOCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
DR Membrane; Transmembrane; Transport.
KW SEQUENCE 337 AA; 37762 MW; B406A52B564F3D30 CRC64;

Query Match 43.0%; Score 726.5; DB 5; Length 337;
Best Local Similarity 44.5%; Pred. No. 1.3e-53;
Matches 143; Conservative 68; Mismatches 99; Indels 11; Gaps 4;

QY 5 ESEER-----LLPLTQWPRASKFLLSGCAATVAELATFPDLTKTQLWQGEAALRLGD 60
DB 18 EKEKPKLEYLVNKKTPPEVLYLTAFASACSAEIVGYPDFDMCKTRKQGEA-SRVG- 75
QY 61 GARESAFYRGMVKTALGIIEEGFLKMOGVTPAIYRHHVYSGRMVTVYHLEHREVFGKS 120
DB 76 ---QKAKYRGLLATANGIVREESGLLYGYSANLFRHLSFGSIKMLTYDYMREKIMVDP 132
QY 121 EDEHYPL--WKSIVGMAGVIGQFLANPTDLVKVQMQEGRKLEKGLRFRGVHHAFA 178
DB 133 EDGRPOLSGFLSGISGVLAGATASVLTNPTELKIQVQMQEGRRLRGEPPRIHNVQLALT 192
QY 179 KILAEGRIGRLWAGVWPNIORAALVNMGDLTYTVKHYLVNTPLEDNINTHGLSSLC 238
DB 193 SIYRTGGVGLWKGIVPNTWRSALTIVDGVCYDFCKRFLIAEFDLVDRVQFVAAMTA 252
QY 239 GLVASILGTTPADVTKSRIMNQPRDKQGRGLLYKSSDCLIQAVOGEFMSLYKGFPLPSWL 298
DB 253 GVADAILSLPADVKSIRIMNQPTDEQGRGIHYKGLSGLDCLSLRVREBEGFLMYKGFIPYWM 312
QY 299 RMTPHSMVFWLTYEKIREMSG 319
DB 312 YEEIKRTGASSF 324

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Db 313 RVGPASVVFWMTEQIRRFGR 333
RESULT 11
Q9X174
ID Q9X174 PRELIMINARY; PRT; 305 AA.
AC Q9X174
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F7A19.22 protein (Putative mitochondrial uncoupling protein).
GN F7A19.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RC STRAIN=cv. Columbia;
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RC STRAIN=cv. Columbia;
RA Haas B.J., Volfovsky N., Town C.D., Troughan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
[3]
RN [3]
RC STRAIN=cv. Columbia;
RA Prover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL "Full-length cDNA from Arabidopsis thaliana.";
DR EMBL; AC007576; AAD39300.1; -
DR ENBL; AY084432; AAM61005.1; -
DR PIR; H86274; H86274.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006839; P:mitochondrial transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mit carrier.
DR InterPro; IPR002030; Mit uncoupling.
DR Pfam; PF00153; mito carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCARRIER; 3.
SQ SEQUENCE 305 AA; 3344 MW; C1122C9B86BC32A CRC64;
Query Match 39.5%; Score 667.5; DB 10; Length 305;
Best Local Similarity 42.5%; Pred. No. 1.2e-48;
Matches 137; Conservative 68; Mismatches 84; Indels 33; Gaps 8;
QY 13 LTRWPFRASKFLSSGCAATVAELATPDLTKTRLMQGEAALA---RLGDGAREAPYR 69
Db 6 VTREPTGTRILLASLSAMVAESVTFPDLTKTRMLQHGSGSAGAHRIQ-----55
QY 70 GMYRTALGIERE---EGFLKLMOGVTPAIYRHVVYSGGRMVTYEHLEVRVFKSE---D 122
Db 56 -----AFGVVSEIARKEGVGLYKGLSPALIRLFYTPRIIGVLENLKLIV-RSETNNS 109
QY 123 EHYPL-WKSVGMAGVIGQFLANPTDLTKVQWMEGKRKLEKGLPRFGVHFAKIL 191
Db 110 ESUPLATKALVGG-FSGVIAQVVASPADLVKVRMQADGRLVSQLGRVPSGPIEAFTKIL 168
182 AEGGIRGLWAGWVPNTQRAALVNMGLTYYDTVKHYLVLTNPTEEDNIMTHGLSLCSGLV 241
169 QSEGVKGLWKGVLPTNQRAFLVNMGLACYDHAKHFVIDKKIAEDNIFAHITLASIMSGLA 228
242 ASILGTPADVIKSRINNQPRDKQGRLLYKSSYDCLIQAVQGGFMSLYKGFPSWLRMT 301
229 STLSLCPADVVKTRMWN-----QGENAVYRNSYDCLVKTVKFGIRGLWKGFPPTWARLG 283
302 PWSMFWLTYEKIREMSGVSPF 323
284 PQQFVFWVSYKEFRLLAGISSF 305
RESULT 12
Q7XTC5
ID Q7XTC5 PRELIMINARY; PRT; 314 AA.
AC Q7XTC5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNBA0064H22.22 protein.
GN OSJNBA0064H22.22.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RC SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606448; CAE01572.1; -
SQ SEQUENCE 314 AA; 33541 MW; 673CBB155B84F1A3 CRC64;
Query Match 37.4%; Score 632; DB 10; Length 314;
Best Local Similarity 42.5%; Pred. No. 1.3e-45;
Matches 127; Conservative 61; Mismatches 95; Indels 16; Gaps 4;
QY 21 SKFLSGCAATVAELATPDLTKTRLMQGEAALRLDGCARESAFYRGWVTRALGIE 80
Db 22 AKVLSLSLAAAAAATFPIDAVKTRLELHRTGSGSGGGG-----GVMRVAGELVR 73
QY 81 EEGFLKLMOGVTPAIYRHVVYSGGRMVTYEHLEVRVFKSEDEHYPLWKSIVGMMAGVI 140
Db 74 DGG---IYRGLSPAVLRHLFYTPRLIRVGHLEHSTFASGGDA--GLLEKALAGVSGVV 128
QY 141 GQFLANPTDLVKVQWMEGKRKLEKGLPRFGVHFAKILAEGLGIRGLWAGWVPNTQRA 200
Db 129 AQVVASPADLVKVRMQADSRLLSQIGQIPRYTGTFDAFTKIVRAEGPRLWKGVPVNAQA 188
QY 201 ALVNMGLTYYDTVKHYLVLTNPTEEDNIMTHGLSSLSLCSGLVASILGTADVKSIRINQ 260
Db 189 FLVNMGLTYYDQAKHFIIRKQICGNDLVAHTLASVAGLSATLSCPADVIKTRMNOG 248
QY 261 RDQGRGLYKSSYDCLIQAVQGGFMSLYKGFPSWLRMTYHLEVRVFKSEDEHYPLWKSIVGMMAGVI 319
Db 249 KDAK---VLYRNSYDCLVKTRVHEGLTALWKGLPTWARLGPWQFVFWVSYEKLQKQASG 304
RESULT 13
Q9CR58
ID Q9CR58 PRELIMINARY; PRT; 291 AA.
AC Q9CR58
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 03:58:39 ; Search time 4096 Seconds
(without alignments)
10994.485 Million cell updates/sec

Title: US-09-397-342C-2
Perfect score: 1039
Sequence: 1 ccgagctcgatcccgcttat.....cagatattccatcacactggc 1039

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
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- 16: em.fun.*
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- 23: em.pat.*
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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1039	100.0	1039	6	BD233771	BD233771 UCP4. 7/2
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3	998	96.1	998	6	AX697337	AX697337 Sequence
4	998	96.1	998	9	AY358711	AY358711 Homo sapi
5	990.6	95.3	1248	6	BD233774	BD233774 UCP4. 7/2
6	972	93.6	972	6	AX269363	AX269363 Sequence
7	972	93.6	972	9	AF110532	AF110532 Homo sapi
8	793	76.3	2851	10	AB106930	AB106930 Mus muscu
9	785	75.6	2678	10	RNO300162	AJ300162 Rattus no
10	729.6	70.2	1339	9	BC033091	BC033091 Homo sapi
11	716.8	69.0	1890	10	RNO300164	AJ300164 Rattus no
12	715.2	68.8	2620	10	RNO300163	AJ300163 Rattus no
13	676.8	65.1	1726	6	AX061217	AX061217 Sequence
14	676.8	65.1	3266	6	AX746657	AX746657 Sequence
15	676.8	65.1	3266	9	AK090871	AK090871 Homo sapi
16	435.8	41.9	1295	5	BC053139	BC053139 Danio rer
17	322.6	31.0	2118	3	AK114236	AK114236 Ciona int
18	234.8	22.6	1546	3	AK115101	AK115101 Ciona int
19	194.6	18.7	18042	9	AL590794	AL590794 Human DNA
20	194.6	18.7	95107	9	AL591242	AL591242 Human DNA
21	165.8	16.0	228	6	AX331480	AX331480 Sequence
22	156.6	15.1	200860	2	AC112993	AC112993 Mus muscu
23	156.6	15.1	237804	2	AC120552	AC120552 Mus muscu
24	150.2	14.5	227939	2	AC125648	AC125648 Rattus no
25	150.2	14.5	229218	2	AC107523	AC107523 Rattus no
26	150.2	14.5	233492	2	AC111723	AC111723 Rattus no
27	140	13.5	1071	8	AY084432	AY084432 Arabidops
28	137.2	13.2	1315	8	AK064234	AK064234 Oryza sat
29	136.6	13.1	945	6	AX653527	AX653527 Sequence
30	134	12.9	566	9	HS3334577	AJ3334577 Homo sapi
31	134	12.9	567	9	HS3334578	AJ3334578 Homo sapi
32	132.4	12.7	1209	8	AB088762	AB088762 Helicodic
33	130.8	12.6	1126	8	AK105976	AK105976 Oryza sat
34	130.6	12.6	147214	8	OSUN00013	AL608448 Oryza sat
35	124	11.9	1083	8	AK117673	AK117673 Arabidops
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37	117.4	11.3	1525	6	E50743	E50743 Plant exoth
38	117.4	11.3	1525	6	BD011855	BD011855 Thermogen
39	117.4	11.3	1525	8	AB024733	AB024733 Symplocar
40	116.2	11.2	1434	8	STUCPMRNA	Y11250 Solanum tub
41	116	11.2	169457	2	AC009216	AC009216 Drosophil
42	116	11.2	169856	3	AC012162	AC012162 Drosophil
43	116	11.2	302073	3	AE003506	AE003506 Drosophil
44	115	11.1	1240	8	ATMTUNCOU	AJ001264 Arabidops
45	114.6	11.0	1429	8	AF472619	AF472619 Lycopersi

ALIGNMENTS

RESULT 1
BD233771
LOCUS BD233771 linear PAT 17-JUL-2003
DEFINITION UCP4.
ACCESSION BD233771
VERSION BD233771.1 GI:33043541
KEYWORDS JP 2002526075-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Adams,S., Fan,J. and Zhong,A.
TITLE UCP4
JOURNAL Patent: JP 2002526075-A 1 20-AUG-2002;

Db 181 AAGCAGCTCTTGCTCGTGGGAGACGGTCAAGAGAAATCTGCCCTATAGGGGAATGG 240
 Qy 254 TGGCAGCAGCCCTAGGATCATTTGAAGAGAGAGGCTTTAAAGCTTTTGGCAAGGAGTGA 313
 Db 241 TGGCAGCAGCCCTAGGATCATTTGAAGAGAGAGGCTTTTAAAGCTTTTGGCAAGGAGTGA 300
 Qy 314 CACCCGCAATTTACAGACACGTAGTGTATTTCTGGAGGTCAATGGTGCATATATGAACATC 373
 Db 301 CACCCGCAATTTACAGACACGTAGTGTATTTCTGGAGGTCAATGGTGCATATATGAACATC 360
 Qy 374 TCCGAGAGGTGTGTTGGGCAAAAGTCAAGATGAGCATTTATCCCTTTGGAATCAGTCA 433
 Db 361 TCCGAGAGGTGTGTTGGGCAAAAGTCAAGATGAGCATTTATCCCTTTGGAATCAGTCA 420
 Qy 434 TTGGAGGATGATGGCTGTGTTATTTGGCCAGTCTTTTAGGCAATCCAACTGACCTAGTGA 493
 Db 421 TTGGAGGATGATGGCTGTGTTATTTGGCCAGTCTTTTAGGCAATCCAACTGACCTAGTGA 480
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 VERSION AX697337.1 GI:29498472
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Ferrar, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
 Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,
 Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A., and Watanabe, C.K.
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JOURNAL Patent: WO 0078961-A 405 28-DEC-2000;
 Genentech Inc. (US)
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 DEFINITION AY358711
 ACCESSION AY358711
 VERSION AY358711.1 GI:37182543
 KEYWORDS FLI_CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 998)

AUTHORS

Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
 Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wleand,D., Woods,K.,
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment

TITLE

Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL

PUBMED 12975309

REFERENCE

2 (bases 1 to 998)

AUTHORS

Clark,H.F.

TITLE

Direct Submission

JOURNAL

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES

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ORIGIN

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RESULT 5

BD233774

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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 UCP4.
 BD233774
 BD233774.1 GI:33043544
 JP 2002526075-A/4.
 synthetic construct
 synthetic construct
 artificial sequences.

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REFERENCE 1 (bases 1 to 1248)
AUTHORS Adams,S., Pan,J. and Zhong,A.
TITLE UCP4
JOURNAL Patent: JP 2002526075-A 4 20-AUG-2002;
GENENTECH INC
COMMENT OS Artificial Sequence
PN JP 2002526075-A/4
PD 20-AUG-2002
PF 15-SEP-1999 JP 2000574252
PR 22-SEP-1998 US 60/101279,30-DEC-1998 US 60/114223 PR
16-APR-1999 US 60/129674
PI SEAN ADAMS, JAMES PAN, ALAN ZHONG
PC C12N15/09,A61K45/00,A61P3/00,A61P3/04,C07K14/47,C07K16/18, PC
C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/
68//
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ACCESSION AX269363
VERSION AX269363.1 GI:16542178
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Berry-Lowe,S.L. and Newell,M.K.
TITLE Compositions and methods for regulating metabolism in plants
JOURNAL Patent: WO 0175131-A 10 11-OCT-2001;
University Technology Corporation (US)
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 1 (bases 1 to 972)
 REFERENCE
 AUTHORS Mao, W., Yu, X.X., Zhong, A., Li, W., Brush, J., Sherwood, S.W., Adams, S.H. and Pan, G.
 TITLE UCP4, a novel brain-specific mitochondrial protein that reduces membrane potential in mammalian cells
 JOURNAL FEBS Lett. 443 (3), 326-330 (1999)
 MEDLINE 99148824
 PUBMED 10025957
 REFERENCE 2 (bases 1 to 972)

AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source

Pan, G., Mao, W., Zhong, A. and Brush, J.
 Direct Submission

Submitted (02-DEC-1998) Endocrinology, Genentech, Inc., 1 DNA Way,
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Query Match 93.6%; Score 972; DB 9; Length 972;
 Best Local Similarity 100.0%; Pred. No. 6,9e-268;
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 Db 61 AGCAAAATCTACTGTCCGCTGCGCGCTTACCGTGGCGGAGTACGACCTTTCCTTCCCTG 120
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 QY 220 GGTGCAAGAGATCTGCCCCCTATAGGGAATGGTGGCAGACACCCCTAGGATCATTTGAA 279
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Qy 1000 AGTCCATTPTAA 1011
Db 961 AGTCCATTPTAA 972

RESULT 8
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LOCUS      2851 bp      mRNA      linear      ROD 29-MAR-2003
DEFINITION Mus musculus UCP4 mRNA for uncoupling protein 4, complete cds.
ACCESSION AB106930
VERSION    AB106930.1 GI:29365510
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1
AUTHORS    Hitomi,Y., Moriya,S., Matsushita,K. and Tanaka,H.
TITLE      Molecular cloning of mouse UCP4 cDNA
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 2851)
AUTHORS    Hitomi,Y., Moriya,S., Matsushita,K. and Tanaka,H.
TITLE      Direct Submission
JOURNAL    Submitted (27-MAR-2003) Yoshinori Hitomi, Utsunomiya University,
          Faculty of Agriculture; 350 Mine-machi, Utsunomiya, Tochigi
          321-8505, Japan (E-mail:hitomik@cc.utsunomiya-u.ac.jp,
          Tel:81-28-649-5465, Fax:81-28-649-5401)
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gene
CDS
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ORIGIN
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Best Local Similarity 89.1%; Pred. No. 2.2e-216;
Matches 854; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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Qy 175 CGACTCCAAATGCAAGAGAGAGCAGCTCTTGTCTGGTTGGGAGACGGTGCAGAGAACTCT 234
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RESULT 9
RNO300162
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LOCUS RNO300162 2678 bp mRNA linear ROD 06-JAN-2001
 DEFINITION Rattus norvegicus mRNA for uncoupling protein UCP-4 (Ucp-4 gene),
 isoform a.
 ACCESSION AJ300162
 VERSION AJ300162.1 GI:12055539
 KEYWORDS isoform a; Ucp-4 gene; Uncoupling protein UCP-4.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1
 Alberati-Giani, D., Gatti, S., Rial, E., Danel, F., Hauser, N.,
 Bubendorff, C. and Bartfai, T.
 TITLE Three different isoforms of UCP-4 are expressed in rat preoptic
 anterior hypothalamus
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2678)
 AUTHORS Alberati-Giani, D.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-2000) Alberati-Giani D., Pharma Division
 Preclinical Research, CNS, F. Hoffmann-La Roche Ltd.,
 Grenzachstrasse 124, CH 4070 Basel, SWITZERLAND
 Location/Qualifiers
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ORIGIN

Query Match 75.6%; Score 785; DB 10; Length 2678;
 Best Local Similarity 87.6%; Pred. No. 4.3e-214;
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RESULT 10

BC033091
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 DEFINITION Homo sapiens solute carrier family 25, member 27, mRNA (cDNA clone
 MGC:45657 IMAGE:5455903), complete cds.
 ACCESSION BC033091
 VERSION BC033091.1 GI:21620095
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1339)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, K.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1339)

Strausberg, R.

Direct Submission

Submitted (25-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-x@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalios, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 43 Row: 0 Column: 13

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4759285.

FEATURES

Location/Qualifiers

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/notes="Vector: pOTB7"

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Best Local Similarity 99.5%; Pred. No. 3.4e-198;

Matches 732; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 281 TTTGCCGCTGACCCAGAGATGGCCCGAGCAGCAAAATTCCTACTGTCCGGCTGCGCGGC 340

QY 129 TACCGTGGCGGAGCTAGCAACCTTTCCCTGGATCTCACAAAAAATCGACTCCAAATGCA 188

DB 341 TACCGTGGCGGAGCTAGCAACCTTTCCCTGGATCTCACAAAAAATCGACTCCAAATGCA 400

QY 189 AGGAGAGCAGCTCTTCTCGCTGGTGGAGACGGTGCAGAGATCTCCCGCTATAGGGG 248

DB 401 AGGAGAGCAGCTCTTCTCGCTGGTGGAGACGGTGCAGAGATCTCCCGCTATAGGGG 460

QY 249 AATGTGTGCGCAGACCGCTTAGGGATCAATGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGG 308

DB 461 AATGTGTGCGCAGACCGCTTAGGGATCAATGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGG 520

QY 309 AGTGACACCGCGCATTTACAGACACGTAGTGTATTTGAGGAGTGAATGGTGCACATATGA 368

DB 521 AGTGACACCGCGCATTTACAGACACGTAGTGTATTTGAGGAGTGAATGGTGCACATATGA 580

QY 369 ACATCTCCAGAGAGTTGTGTTGGCAAAAGTGAAGATGACATATCCCTTTGGAAATC 428

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QY 429 AGTCATTGAGGAGATGATCGCTGTTATTTGGCCAGTTTATAGCCAATCCAATGACCT 488

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QY 609 GGCAGGCTGGGTACCCCAATATACAAAGAGCAGCACCTGGTGAATATCGGAGATTTAACAC 668

DB 821 GGCAGGCTGGGTACCCCAATATACAAAGAGCAGCACCTGGTGAATATCGGAGATTTAACAC 880

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DB 881 TTATGATACAGTGAACACACTACTTGGTATTTGAATACACCACTTTGAGGACAATATCATGAC 940

QY 729 TCACGGTTTATCAAGT 744

DB 941 TCACGGTTTATCAAGT 956

RESULT 11

LOCUS RNO300164

DEFINITION Rattus norvegicus mRNA for uncoupling protein UCP-4 (Ucp-4 gene)

ACCESSION AJ300164

VERSION AJ300164.1 GI:12055543

KEYWORDS isoform c; Ucp-4 gene; Uncoupling protein UCP-4.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

Alberati-Giani, D., Gatti, S., Rial, E., Danel, F., Hauser, N.,
Bubendorff, C. and Bartfai, T.

TITLE

Three different isoforms of UCP-4 are expressed in rat preoptic
hypothalamus

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1890)

AUTHORS

Alberati-Giani, D.

TITLE

Direct Submission

JOURNAL

Submitted (02-NOV-2000) Alberati-Giani D., Pharma Division

FEATURES

source

Location/Qualifiers
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CDS

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ORIGIN

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LOCUS
DEFINITION
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isoform b.
AJ300163
VERSION
AJ300163.1 GI:12055541
KEYWORDS
isoform b; Ucp-4 gene; Uncoupling protein UCP-4.
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Rattus.
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REFERENCE
AUTHORS
Alberati-Giani, D., Gatti, S., Rial, E., Danel, F., Hauser, N.,
Bubendorff, C. and Bartfai, T.
TITLE
Three different isoforms of UCP-4 are expressed in rat preoptic
anterior hypothalamus
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2620)
AUTHORS
Alberati-Giani, D.
TITLE
Direct Submission
JOURNAL
Submitted (02-NOV-2000) Alberati-Giani D., Pharma Division
Preclinical Research, CNS, F. Hoffmann-La Roche Ltd.,
Grenzacherstrasse 124, CH 4070 Basel, SWITZERLAND
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Best Local Similarity 86.8%; Pred. No. 5e-194;
Matches 799; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

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ACCESSION AX061217
VERSION AX061217.1 GI:12406353
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lal, P., Yang, J., Yue, H., Hillman, J. L., Tang, Y. T., Bandman, O.,
Burford, N., Baughn, M. R., Azimzai, Y., Lu, D. A., Au-Young, J. and
Patterson, C.
TITLE Human transport proteins
JOURNAL Patent: WO 0078953-A 64 28-DEC-2000;
Incyte Genomics, Inc. (US)
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Best Local Similarity 99.7%; Pred. No. 5.3e-183;
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 VERSION AX746657.1 GI:32130924
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
 Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
 Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
 Masuho, Y.
 TITLE Full-length cDNA sequences
 JOURNAL Patent: EP 1308459-A 182 07-MAY-2003;
 Helix Research Institute (JP); Research Association for
 Biotechnology (JP)
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 VERSION AK090871.1 GI:21749113
 KEYWORDS oligo capping; fis (full insert sequence).
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
 Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R.,
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J. I., Isono, Y.,
 Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
 Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
 Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
 Nagahari, K., Masuho, Y., Nagai, K. and Isegai, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 3266)
 Isegai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isegai, FLJ Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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 Evaluation; clone selection for full insert sequencing: HRI and
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Best Local Similarity 99.7%; Pred. No. 5.6e-183;
Matches 678; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 03:57:38 ; Search time 453 Seconds

(without alignments)
9743.660 Million cell updates/sec

Title: US-09-397-342C-2

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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- 2: Geneseqn1990s:*
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- 8: Geneseqn2003bs:*
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SUMMARIES

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9	998	96.1	998	7	AB174440 Human CDN
10	998	96.1	998	7	AB174440 Novel hum
11	998	96.1	998	7	AB174440 Human CDN
12	998	96.1	998	7	AB174440 Novel hum
13	998	96.1	998	7	AB174440 Human CDN
14	998	96.1	998	7	AB174440 Novel hum
15	998	96.1	998	7	AB174440 Human CDN
16	998	96.1	998	7	AB174440 Novel hum
17	998	96.1	998	7	AB174440 Human CDN
18	998	96.1	998	7	AB174440 Novel hum
19	998	96.1	998	7	AB174440 Human CDN
20	998	96.1	998	7	AB174440 Novel hum
21	998	96.1	998	8	AB17182 Human CDN
22	998	96.1	998	8	AB17182 Human sec
23	998	96.1	998	8	AB17182 Novel hum

24	998	96.1	998	8	ADA19987	ADA19987 Novel hum
25	998	96.1	998	8	ADA17370	ADA17370 Human CDN
26	998	96.1	998	8	ADA20159	ADA20159 Novel hum
27	998	96.1	998	8	ADA20152	ADA20152 Human sec
28	998	96.1	998	8	ADA00456	ADA00456 Human sec
29	998	96.1	998	8	ACH04628	ACH04628 Human CDN
30	998	96.1	998	8	ACH04628	ACH04628 Novel hum
31	998	96.1	998	8	ACH04628	ACH04628 Novel hum
32	998	96.1	998	8	ACH04628	ACH04628 Novel hum
33	998	96.1	998	9	ACH04628	ACH04628 Human PRO
34	998	96.1	998	9	ACH04628	ACH04628 Novel hum
35	998	96.1	998	9	ACH04628	ACH04628 Novel hum
36	998	96.1	998	9	ACH04628	ACH04628 Novel hum
37	998	96.1	998	9	ACH04628	ACH04628 Novel hum
38	998	96.1	998	9	ACH04628	ACH04628 Novel hum
39	998	96.1	998	9	ACH04628	ACH04628 Novel hum
40	998	96.1	998	9	ACH04628	ACH04628 Novel hum
41	998	96.1	998	9	ACH04628	ACH04628 Novel hum
42	998	96.1	998	9	ACH04628	ACH04628 Novel hum
43	998	96.1	998	9	ACH04628	ACH04628 Novel hum
44	998	96.1	998	9	ACH04628	ACH04628 Novel hum
45	998	96.1	998	9	ACH04628	ACH04628 Novel hum

ALIGNMENTS

RESULT 1
AA14084
ID AA14084 standard; cDNA; 1039 BP.
XX
AC AA14084;
XX
DT 21-JUL-2000 (first entry)
XX
DE cDNA encoding human uncoupling protein UCP4.

XX
KW Uncoupling protein; UCP4; expressed sequence tag; EST; human;
KW Chromosome 6p11.2-q12; ATP synthesis; energy efficiency;
KW Mitochondrial membrane; proton leakage; heat production; metabolic rate;
KW drug screening; obesity; stroke; trauma; sepsis; infection; ss.

OS Homo sapiens.
FH Key
FT CDS
FT Location/Qualifiers
FT 40..1011
FT /*tag= a
FT /product= "Human UCP4"

XX
XX WO200017353-A1.
XX
XX 30-MAR-2000.
XX
XX 15-SEP-1999; 99WO-US021194.
XX
XX 22-SEP-1998; 98US-0101279P.
XX
XX 30-DEC-1998; 98US-0114223P.
XX
XX 16-APR-1999; 99US-0129674P.

XX (GETH) GENENTECH INC.

XX Adams S, Pan J, Zhong A;

XX WPI; 2000-292842/25.

XX P-PSDB; AAY81497.

XX New nucleic acid encoding human uncoupled protein-4, useful e.g for
XX identifying metabolic regulators for treatment of obesity.

XX Claim 3; Fig 2; 80pp; English.

XX This sequence represents cDNA encoding human uncoupling protein UCP4. The
XX human UCP4 cDNA (ATCC 203134) was isolated from a brain cDNA library

PR 15-SEP-1998; 98US-0100330P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101071P.
 PR 23-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
 PR 07-OCT-1998; 98US-0103315P.
 PR 07-OCT-1998; 98US-0103328P.
 PR 07-OCT-1998; 98US-0103395P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 07-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103779P.
 PR 08-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105693P.
 PR 26-OCT-1998; 98US-0105694P.
 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105881P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 28-OCT-1998; 98US-0106062P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.

PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 18-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-237871/20.
 DR P-PSDB; AAY99457.
 XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX
 PS Claim 2; Fig 235; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 3; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CCGTTATCGTTCGCGCTACTGCTGAATGTCCTCCCGAGGAGGAGGAGGCTTTTCG 73
 |||||
 Db 1 CCGTTATCGTTCGCGCTACTGCTGAATGTCCTCCCGAGGAGGAGGAGGCTTTTCG 60
 |||||
 Qy 74 CGCTGACCCAGAGATGCCCGGAGGAGCAAAATTCCTACTGTCCGGTCCGGCTACCG 133
 |||||
 Db 61 CGCTGACCCAGAGATGCCCGGAGGAGCAAAATTCCTACTGTCCGGTCCGGCTACCG 120
 |||||
 Qy 134 TGGCCGAGCTAGCAACTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 193
 |||||
 Db 121 TGGCCGAGCTAGCAACTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 180
 |||||
 Qy 194 AAGCAGCTTTGCTCGGTGGGAGCGGTCAAGAGAAATCTGCCCCCTATAGGGGAATGG 253
 |||||
 Db 181 AAGCAGCTTTGCTCGGTGGGAGCGGTCAAGAGAAATCTGCCCCCTATAGGGGAATGG 240
 |||||

QY 674 ATACAGTGAACACTACTCTGGTATTGATGATACACCACTTGAGGACAATATCATGACTCAAG 733
 Db 661 ATACAGTGAACACTACTCTGGTATTGATGATACACCACTTGAGGACAATATCATGACTCAAG 720
 QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTCTTATCTTGGGAACACCAAGGCGGATGTCA 793
 Db 721 GTTTATCAAGTTTATGTTCTGGACTGGTCTTATCTTGGGAACACCAAGGCGGATGTCA 780
 QY 794 TCAAAACGAGAATATGAATCAACCAACGAGATAAACAAGGAAGGGGACTTTTGTATATAAT 853
 Db 781 TCAAAACGAGAATATGAATCAACCAACGAGATAAACAAGGAAGGGGACTTTTGTATATAAT 840
 QY 854 CATCGACTGACTGCTTCAATCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 913
 Db 841 CATCGACTGACTGCTTCAATCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 900
 QY 914 GCTTTTACCACATCTTGCTGAGATGACCCCTTGCTCAATGGTCTTCTGGCTTACTTATG 973
 Db 901 GCTTTTACCACATCTTGCTGAGATGACCCCTTGCTCAATGGTCTTCTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGATGAGTGGAGTCACTAGTCAATTTAA 1011
 Db 961 AAAAAATCAGAGATGAGTGGAGTCACTAGTCAATTTAA 998
 RESULT 5
 ABS74440
 ID ABS74440 standard; cdna; 998 BP.
 XX
 AC ABS74440;
 XX
 AC ABS74440;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 XX Human cDNA encoding secreted/transmembrane protein PRO1566.
 DE Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 XX US2002119130-A1.
 XX
 XX 29-AUG-2002.
 XX
 XX 06-DEC-2001; 2001US-00006867.
 XX
 XX 29-OCT-1997; 97US-0063435P.
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 XX 29-OCT-1997; 97US-0064215P.
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 XX 22-APR-1998; 98US-0082797P.
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 XX 23-APR-1998; 98US-0083495P.
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 XX 02-JUN-1998; 98US-0087759P.
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 XX 04-JUN-1998; 98US-0088021P.
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 XX 04-JUN-1998; 98US-0088029P.
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 XX 04-JUN-1998; 98US-0088030P.
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 XX 10-JUN-1998; 98US-0088734P.
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 XX 10-JUN-1998; 98US-0088740P.
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 XX 10-JUN-1998; 98US-0088811P.
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 XX 10-JUN-1998; 98US-0088824P.
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 XX 10-JUN-1998; 98US-0088825P.
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 XX 11-JUN-1998; 98US-0088863P.
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 XX 12-JUN-1998; 98US-0089105P.
 XX
 XX 16-JUN-1998; 98US-0089514P.
 XX
 XX 17-JUN-1998; 98US-0089653P.
 XX
 XX 19-JUN-1998; 98US-0089952P.
 XX
 XX 22-JUN-1998; 98US-0090246P.
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 XX 24-JUN-1998; 98US-0090444P.
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 XX 25-JUN-1998; 98US-0090688P.
 XX
 XX 25-JUN-1998; 98US-0090862P.
 XX
 XX 26-JUN-1998; 98US-0090862P.
 XX
 XX 02-JUL-1998; 98US-0091628P.

PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 16-SEP-1998; 98US-0100827P.
 PR 16-SEP-1998; 98US-0100862P.
 PR 16-SEP-1998; 98US-0100863P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski EJ;
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2002-731348/79.
 P-PSDB; ABG95913.

New isolated secreted and transmembrane PRO polypeptide useful for
 modulating biological activity of a cell, or for treating sports-related
 joint problems, osteoarthritis or rheumatoid arthritis.

Claim 2; Fig 125; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
 polypeptide having 80 % sequence identity to a sequence appearing as
 ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 extracellular domain of the proteins with their associated signal peptide
 or lacking its associated signal peptide. Also included are the nucleic
 acids encoding the proteins, vectors, host cells, fusion proteins and

PR	18-JUL-2001; 2001US-00908827.	Db	481	AGGTTTCAGATGCAATGGAAGGAAAAAGGAAATCGGAAGAAACCAATCCGATTTTCGTG	540
XX	06-DEC-2001; 2001US-00006867.	QY	554	GTGTACATCATGCTATTGCAAAAATCTTAGCTCAAGGAGGAATACAGAGGCTTTTGGGCGAG	613
PA	(GETH) GENENTECH INC.	Db	541	GTGTACATCATGCTATTGCAAAAATCTTAGCTCAAGGAGGAATACAGAGGCTTTTGGGCGAG	600
XX	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;	QY	614	GCTGGGTACCCCAATATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG	673
PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;	Db	601	GCTGGGTACCCCAATATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG	660
XX	P-PSDB; ABO33997.	QY	674	ATACAGTGAACACACTCTTGGTATTGAATACACCACTTGGGAGCAATATCATGACTCAGC	733
PT	New isolated antibody specifically binding a PRO polypeptide, useful for	Db	661	ATACAGTGAACACACTCTTGGTATTGAATACACCACTTGGGAGCAATATCATGACTCAGC	720
PT	the preparation of a medicament for treating disorders with the aberrant	QY	734	GTTTATCAAGTTTATGTTCTGGACTCGTAGCTTCTATTCTGGGAAACACAGCCGATGTCA	793
PT	expression or activity of the PRO polypeptide, such as tumor conditions	Db	721	GTTTATCAAGTTTATGTTCTGGACTCGTAGCTTCTATTCTGGGAAACACAGCCGATGTCA	780
XX	and cancer.	QY	794	TCAAAAGCAGAATAATGAATCAACACGAGATTAACAAGGAGGACTTTTGTATAAAT	853
PS	Disclosure; Fig 125; 223pp; English.	Db	781	TCAAAAGCAGAATAATGAATCAACACGAGATTAACAAGGAGGACTTTTGTATAAAT	840
XX	The invention relates to an antibody that binds to a secreted or	QY	854	CATCGACTGACTGCTTGGTATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG	913
CC	transmembrane protein designated PRO1446 appearing as ABO33941. The	Db	841	CATCGACTGACTGCTTGGTATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG	900
CC	protein is one of 84 PRO polypeptides which (along with their encoding	QY	914	GCTTTTATCACTCTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG	973
CC	nucleic acids) are disclosed in the specification. The methods and	Db	901	GCTTTTATCACTCTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG	960
CC	compositions of the present invention are useful for the preparation of a	QY	974	AAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011	
CC	medicament for the treatment of disorders associated with the aberrant	Db	961	AAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998	
CC	expression or activity of the PRO polypeptide, such as tumour conditions	QY			
CC	and cancer. They can also be used to generate transgenic or knockout	Db			
CC	animals useful in the development and screening of therapeutically useful	QY			
CC	reagents. The PRO polypeptides and encoding nucleic acids can be used as	Db			
CC	molecular weight markers for protein electrophoresis, chromosome	QY			
CC	identification and tissue typing. The antibodies may be used in various	Db			
CC	diagnostic, competitive binding and/or immunoprecipitation assays. The	QY			
CC	present sequence encodes a PRO polypeptide	Db			
XX	Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;	QY			
SQ		Db			
Query Match	96.1%; Score 998; DB 7; Length 998;	RESULT 8			
Best Local Similarity	100.0%; Pred. No. 0;	ACA60425			
Matches 998; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	ID ACA60425 standard; cDNA; 998 BP.			
QY	14 CCGTTATCGTTCGCGTACTGCTGAATGTCGTCGCGGAGGAGGAGGCGCTTTTGC	XX	ACA60425;		
Db	1 CCGTTATCGTTCGCGTACTGCTGAATGTCGTCGCGGAGGAGGAGGCGCTTTTGC	XX	11-JUN-2003 (first entry)		
QY	74 CGCTGACCCAGAGATGCCCGGAGCGAGCAAAATCTCTACTGTCCGGCTGCGCGGTACCG	DE	Novel human secreted and transmembrane protein PRO1566 cDNA.		
Db	61 CGCTGACCCAGAGATGCCCGGAGCGAGCAAAATCTCTACTGTCCGGCTGCGCGGTACCG	XX	Human; secreted and transmembrane polypeptide; gene;		
QY	134 TGGCCGAGCTAGCAACTTTCCCTCGATCTCAAAAACTCGACTCCAAATGCAAGGAG	KW	ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;		
Db	121 TGGCCGAGCTAGCAACTTTCCCTCGATCTCAAAAACTCGACTCCAAATGCAAGGAG	KW	therapeutic agent screening; chromosome identification; tissue typing;		
QY	194 AAGCAGCTCTTGTCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG	XX	Homo sapiens.		
Db	181 AAGCAGCTCTTGTCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG	OS	US2003018183-A1.		
QY	254 TGGCCACAGCCCTAGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	PN	23-JAN-2003.		
Db	241 TGGCCACAGCCCTAGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	XX	01-MAY-2002; 2002US-00063512.		
QY	314 CACCCGCCAATTTACAGACAGTATGATTTCTGGAGGTGCAATGATGCAATATGAACATC	XX	06-DEC-2001; 2001US-00006867.		
Db	301 CACCCGCCAATTTACAGACAGTATGATTTCTGGAGGTGCAATGATGCAATATGAACATC	XX	(GETH) GENENTECH INC.		
QY	374 TCCGAGAGGTGTTTGGCAAGTGAAGATGAGCAATATCCCTTTGGAATCATGTCA	PI	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;		
Db	361 TCCGAGAGGTGTTTGGCAAGTGAAGATGAGCAATATCCCTTTGGAATCATGTCA	PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;		
QY	434 TTGGAGGAGTATGCTGCTGTTTATTTGGCCAGTCTTTTAGCCAAATCAACTGACTAGTGA	DR	WPI; 2003-330984/31.		
Db	421 TTGGAGGAGTATGCTGCTGTTTATTTGGCCAGTCTTTTAGCCAAATCAACTGACTAGTGA	DR	P-PSDB; ABU72014.		
QY	494 AGGTTTCAGATGCAATGGAAGGAAAAAGGAAATCGGAAGGAAACCAATTCGCGATTTTCGTG	XX	New secreted and transmembrane PRO polypeptides and nucleic acid		
		XX	molecules encoding the polypeptides, useful in gene therapy or preparing		
		XX	a medicament for treating a condition that is responsive to the PRO		
		XX	polypeptide or antibody.		

PS Disclosure; Fig 125; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO
 CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
 CC for treating a condition that is responsive to the PRO polypeptide or
 CC antibody. The PRO nucleotide sequences may be used as hybridisation
 CC probes in chromosome and gene mapping, or in generating antisense RNA and
 CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
 CC assays to identify other proteins or molecules involved in binding
 CC reaction, to generate transgenic animals or knockout animals, which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents, for chromosome identification, and tissue typing. The
 CC PRO polypeptides and nucleic acid molecules are also useful in gene
 CC therapy, and as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. This sequence encodes a novel human secreted
 CC and transmembrane PRO polypeptide

XX Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	14	CCGTTATCGTCTTGGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC	73
Db	1	CCGTTATCGTCTTGGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC	60
QY	74	CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATCTCTACTGTCCGGCTGGCGCTACCG	133
Db	61	CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATCTCTACTGTCCGGCTGGCGCTACCG	120
QY	134	TGGCGGAGCTAGCAACCTTCCCTCGATCTCAAAAACTCGATCTCAAAATGCAAGGAG	193
Db	121	TGGCGGAGCTAGCAACCTTCCCTCGATCTCAAAAACTCGATCTCAAAATGCAAGGAG	180
QY	194	AAGCAGCTCTTGTCTGGTGGGAGACGCTGCAAGAGAAATCTGCCCTATAGGGGAATGG	253
Db	181	AAGCAGCTCTTGTCTGGTGGGAGACGCTGCAAGAGAAATCTGCCCTATAGGGGAATGG	240
QY	254	TGCCACAGCCCTAGGATCATTTGAAGAGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
Db	241	TGCCACAGCCCTAGGATCATTTGAAGAGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
QY	314	CACCCGCAATTACAGACAGTGTATCTGAGGTGCAATGGTCAATATGAACATC	373
Db	301	CACCCGCAATTACAGACAGTGTATCTGAGGTGCAATGGTCAATATGAACATC	360
QY	374	TCCGAGAGTGTGTGGCAAAAGTGAAGATGAGCATATATCCCTTTTGAAATCAGTCA	433
Db	361	TCCGAGAGTGTGTGGCAAAAGTGAAGATGAGCATATATCCCTTTTGAAATCAGTCA	420
QY	434	TTGGAGGATGATGGCTGTGTATTTGGCCAGTCTTTAGCCATCCAACTGACCTAGTGA	493
Db	421	TTGGAGGATGATGGCTGTGTATTTGGCCAGTCTTTAGCCATCCAACTGACCTAGTGA	480
QY	494	AGGTTACAGATGCAATGGAAGGAAAGGAAATCGGAAGAAACCAATTCGCAATTCGTG	553
Db	481	AGGTTACAGATGCAATGGAAGGAAAGGAAATCGGAAGAAACCAATTCGCAATTCGTG	540
QY	554	GTGTACATCATGATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGCTTTGGGCGAG	613
Db	541	GTGTACATCATGATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGCTTTGGGCGAG	600
QY	614	GCTGGGTACCAATATACAAAGAGCAGCTGCTGTAATGAGGATTTAAACCACTATG	673
Db	601	GCTGGGTACCAATATACAAAGAGCAGCTGCTGTAATGAGGATTTAAACCACTATG	660
QY	674	ATACAGTGAACACTACTTGGTATTGAATACACCACTTTGAGGACAATATCATGACTCAG	733
Db	661	ATACAGTGAACACTACTTGGTATTGAATACACCACTTTGAGGACAATATCATGACTCAG	720

QY	734	GTTTATCAAGTTTATGTTCTGGACTGCTAGCTTCTATTCTGGGAACACACAGCCGATGTC	793
Db	721	GTTTATCAAGTTTATGTTCTGGACTGCTAGCTTCTATTCTGGGAACACACAGCCGATGTC	780
QY	794	TCAAAAGCAGAAATGAATCAACACGAGATAAACAAAGAGGAGGACTTTTGTATAAAT	853
Db	781	TCAAAAGCAGAAATGAATCAACACGAGATAAACAAAGAGGAGGACTTTTGTATAAAT	840
QY	854	CATCGACTGACTCTTGAATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATAAAG	913
Db	841	CATCGACTGACTCTTGAATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATAAAG	900
QY	914	GCCTTTTACCACCTTGGCTGAGATCAACCCCTTGGTCAATGGTCTTGGCTTACTTATG	973
Db	901	GCCTTTTACCACCTTGGCTGAGATCAACCCCTTGGTCAATGGTCTTGGCTTACTTATG	960
QY	974	AAAAAATCAGAGATGAGTGGAGTCAAGTCCAGTCCATTTAA	1011
Db	961	AAAAAATCAGAGATGAGTGGAGTCAAGTCCAGTCCATTTAA	998
RESULT 9			
ACA58872			
ID	ACA58872 standard; cDNA; 998 BP.		
XX	ACA58872;		
AC	ACA58872;		
XX	ACA58872;		
DT	10-JUN-2003 (first entry)		
XX	cDNA encoding human secreted polypeptide PRO1566.		
DE	Human; ss; gene; gene therapy; tumour; cancer.		
KW	Human; ss; gene; gene therapy; tumour; cancer.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	US2003013855-A1.		
PN	16-JAN-2003.		
XX	03-MAY-2002; 2002US-00063616.		
PF	30-DEC-1998; 98KR-00062142.		
XX	08-MAR-1999; 99WO-US0005028.		
PR	14-MAY-1999; 99US-00311832.		
PR	14-MAY-1999; 99WO-US010733.		
PR	25-AUG-1999; 99US-00380137.		
PR	25-AUG-1999; 99US-00380138.		
PR	25-AUG-1999; 99US-00380139.		
PR	25-AUG-1999; 99US-00380142.		
PR	15-SEP-1999; 99US-00397342.		
PR	18-OCT-1999; 99US-00403297.		
PR	12-NOV-1999; 99US-00423844.		
PR	30-DEC-1999; 99WO-US01274.		
PR	18-FEB-2000; 2000WO-US004341.		
PR	01-MAR-2000; 2000WO-US005601.		
PR	02-MAR-2000; 2000WO-US005841.		
PR	21-MAR-2000; 2000WO-US007532.		
PR	02-JUN-2000; 2000WO-US014042.		
PR	22-AUG-2000; 2000US-00644848.		
PR	24-AUG-2000; 2000WO-US023328.		
PR	18-SEP-2000; 2000US-00664610.		
PR	18-SEP-2000; 2000US-00665350.		
PR	08-NOV-2000; 2000US-00709238.		
PR	10-NOV-2000; 2000WO-US030873.		
PR	01-DEC-2000; 2000WO-US032678.		
PR	20-DEC-2000; 2000US-00747259.		
PR	20-DEC-2000; 2000WO-US034956.		
PR	28-FEB-2001; 2001WO-US006520.		
PR	22-MAR-2001; 2001US-00816744.		
PR	10-MAY-2001; 2001US-00854208.		
PR	10-MAY-2001; 2001US-00854280.		
PR	30-MAY-2001; 2001US-00870574.		

30-DEC-1999; 99WO-US031274.
 18-FEB-2000; 2000WO-US04341.
 01-MAR-2000; 2000WO-US05601.
 02-MAR-2000; 2000WO-US005841.
 21-MAR-2000; 2000WO-US007532.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 22-AUG-2000; 2000US-00644848.
 24-AUG-2000; 2000WO-US023328.
 18-SEP-2000; 2000US-00664610.
 18-SEP-2000; 2000US-00665350.
 08-NOV-2000; 2000US-00709238.
 10-NOV-2000; 2000WO-US030873.
 01-DEC-2000; 2000WO-US032878.
 20-DEC-2000; 2000US-00747259.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US006520.
 22-MAR-2001; 2001US-00816744.
 10-MAY-2001; 2001US-00854208.
 30-MAY-2001; 2001US-00870574.
 01-JUN-2001; 2001WO-US017800.
 05-JUN-2001; 2001US-00874503.
 29-JUN-2001; 2001US-00869599.
 18-JUL-2001; 2001US-00908827.
 06-DEC-2001; 2001US-00006867.
 (GETH) GENENTECH INC.
 Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 WPI; 2003-328612/04.
 P-PSDB; ABU72349.
 An isolated secreted transmembrane polypeptide designated PRO, useful as
 a therapeutic agent.
 Disclosure; Fig 125; 236pp; English.
 The present invention relates to the isolation of novel human PRO
 polypeptides, and the polynucleotide sequences encoding them. The PRO
 polypeptides are secreted and transmembrane proteins. The PRO
 polypeptides and polynucleotides are useful for preparing a medicament
 useful in the treatment of a condition responsive to anti-PRO antibody.
 Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
 its expression in specific cells, tissues or serum, and for affinity
 purification of PRO from recombinant cell culture or natural sources.
 ACA63986-ACA64069 represent cDNA sequences encoding the human PRO
 polypeptides of the invention
 Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;
 Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 14 CCGTTATCGTCTTGGCTACTGCTGAATGTCGTCGCGAGGAGGAGGAGGCTTTTGC 73
 1 CCGTTATCGTCTTGGCTACTGCTGAATGTCGTCGCGAGGAGGAGGAGGCTTTTGC 60
 74 CGCTGACCCAGAGATGCGCGAGCGAGCAAAATTCCTACTGTCGCGTCCGCGCTACCG 133
 61 CGCTGACCCAGAGATGCGCGAGCGAGCAAAATTCCTACTGTCGCGTCCGCGCTACCG 120
 134 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAAAAATCTCGACTTCCAAATCAAGGAG 193
 121 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAAAAATCTCGACTTCCAAATCAAGGAG 180
 194 AGCAGCTCTTGTCTGGTCTGGGAGCGGTCAAGAGAAATCTGCCCTATAGGGGAATGG 253
 181 AAGCAGCTCTTGTCTGGTCTGGGAGCGGTCAAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 254 TCGCACAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGATGA 313
 DB 241 TCGCACAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGATGA 300
 QY 314 CACCCGCCATTATACAGACAGTAGTGTATTCTCGAGGTGAAATGGTCAACATATGAACATC 373
 DB 301 CACCCGCCATTATACAGACAGTAGTGTATTCTCGAGGTGAAATGGTCAACATATGAACATC 360
 QY 374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGATTAATCCCTTTGGAATCAAGTCA 433
 DB 361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGATTAATCCCTTTGGAATCAAGTCA 420
 QY 434 TTGAGGGGATGATGGCTGGTGTATTGGCCAGTTTATAGCCAAATCAACTGACTAGTGA 493
 DB 421 TTGAGGGGATGATGGCTGGTGTATTGGCCAGTTTATAGCCAAATCAACTGACTAGTGA 480
 QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAGAAATCGAAGGAAACCAATTCGCAATTCGTTG 553
 DB 481 AGGTTTCAGATGCAAAATGGAAGGAAAGAAATCGAAGGAAACCAATTCGCAATTCGTTG 540
 QY 554 GTGTATCATGATGCAATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGGCTTTGGGCGAG 613
 DB 541 GTGTATCATGATGCAATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGGCTTTGGGCGAG 600
 QY 614 GCTGGGTACCCATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACATTATG 673
 DB 601 GCTGGGTACCCATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACATTATG 660
 QY 674 ATACAGTGAACACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 733
 DB 661 ATACAGTGAACACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 720
 QY 734 GTTTATCAAGTTTATGTTCTGAGCTGGTAGCTTCTATTCTTGGGAAACACAGCCGATGTCA 793
 DB 721 GTTTATCAAGTTTATGTTCTGAGCTGGTAGCTTCTATTCTTGGGAAACACAGCCGATGTCA 780
 QY 794 TCAAAAGCAGATAATGAATCAACACAGAGATAAACAAGAGGGGACTTTTGTATATAAT 853
 DB 781 TCAAAAGCAGATAATGAATCAACACAGAGATAAACAAGAGGGGACTTTTGTATATAAT 840
 QY 854 CATCGACTGACTGCTTGTATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 913
 DB 841 CATCGACTGACTGCTTGTATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 900
 QY 914 GCTTTTACCAATCTGGCTGAGATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG 973
 DB 901 GCTTTTACCAATCTGGCTGAGATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 1011
 DB 961 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 998
 RESULT 11
 ACA91312
 ID ACA91312 standard; cDNA; 998 BP.
 XX ACA91312;
 AC ACA91312;
 XX
 DT 14-JUL-2003 (first entry)
 XX
 DX cDNA encoding human PRO polypeptide #63.
 DE
 XX Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;
 KW lung; stomach; oesophageal; skin; tumour; cancer; cytostatic;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003018168-A1.
 XX
 PD 23-JAN-2003.
 XX

PF 02-MAY-2002; 2002US-00063569.
 XX 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US0005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-0074259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 29-JUN-2001; 2001US-00869599.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 XX WPI; 2003-401699/38.
 DR P-PSDB; ABU91022.
 DR
 XX
 XX New isolated, secreted and transmembrane PRO polypeptide, useful for the
 PT diagnosis, prevention and treatment of rectal, lung, stomach, esophageal
 PT or skin cancers.
 PT
 XX
 XX Disclosure; Fig 125; 235pp; English.
 PS
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO polypeptide
 CC and polynucleotide sequences are useful for the diagnosis, prevention and
 CC treatment of rectal, lung, stomach, esophageal or skin tumours, and/or
 CC cancers. The PRO polypeptides are also useful as molecular weight
 CC markers. The PRO polynucleotide sequences are useful for chromosome
 CC identification, hybridisation probes, and for screening libraries of
 CC human cDNA, genomic DNA or mRNA. They may also be used in gene therapy,
 CC particularly for replacing a defective gene. ACA91250-ACA91333 represent
 CC cDNA sequences encoding the human PRO polypeptides of the invention
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 14 CCCTTATCGTCTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73

1	CCGTTATCGTCTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC	60
74	CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATCTCTACTGTCCGGCTGCGCGCTACCG	133
61	CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATCTCTACTGTCCGGCTGCGCGCTACCG	120
134	TGGCCGAGCTAGCAACTCTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG	193
121	TGGCCGAGCTAGCAACTCTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG	180
194	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGAAATCTGCCCTTATAGGGGAATGG	253
181	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGAAATCTGCCCTTATAGGGGAATGG	240
254	TGCGCACAGCCCTAGGAGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
241	TGCGCACAGCCCTAGGAGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
314	CACCCGCCATTTACAGACACGTAAGTCTTCTGAGGTGGAATGGTGCACATATGAACATC	373
301	CACCCGCCATTTACAGACACGTAAGTCTTCTGAGGTGGAATGGTGCACATATGAACATC	360
374	TCCGAGAGGTTGTGTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA	433
361	TCCGAGAGGTTGTGTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA	420
434	TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTATGGCCAAATCAACTGACCTAGTGA	493
421	TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTATGGCCAAATCAACTGACCTAGTGA	480
494	AGGTTCCAGATGCAAAATGGAAGGAAAAAGGAAATCGAAGGAAAAACCATTCGCTG	553
481	AGGTTCCAGATGCAAAATGGAAGGAAAAAGGAAATCGAAGGAAAAACCATTCGCTG	540
554	GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAAGAGGAAATACGAGGCTTTGGGAG	613
541	GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAAGAGGAAATACGAGGCTTTGGGAG	600
614	GCTGGGTACCCATATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTTAAACCATTTATG	673
601	GCTGGGTACCCATATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTTAAACCATTTATG	660
674	ATACAGTGAACACACTCTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG	733
661	ATACAGTGAACACACTCTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG	720
734	GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTCTGGGAAACACCGCCGATGCA	793
721	GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTCTGGGAAACACCGCCGATGCA	780
794	TCAAAAGCAGATATGAATCAACAGGAGATTAACAAAGGAGGAGCTTTTGTATTAAT	853
781	TCAAAAGCAGATATGAATCAACAGGAGATTAACAAAGGAGGAGCTTTTGTATTAAT	840
854	CATCGACTGACTGCTTGAATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG	913
841	CATCGACTGACTGCTTGAATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG	900
914	GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	973
901	GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	960
974	AAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011	
961	AAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998	

RESULT 12
 ACD45211 standard; cDNA; 998 BP.
 XX
 AC ACD45211;

XX 11-SEP-2003 (first entry)
 XX Human secreted/transmembrane polypeptide PRO1566 cDNA.
 XX Human; ss; tumour; cancer; gene therapy; tissue typing; gene.
 XX Homo sapiens.
 OS
 PN US2003009012-A1.
 XX 09-JAN-2003.
 XX 01-MAY-2002; 2002US-00063517.
 XX 30-DEC-1998; 98KR-00062142.
 XX 08-MAR-1999; 99WO-US005028.
 XX 14-MAY-1999; 99US-00311832.
 XX 14-MAY-1999; 99WO-US010733.
 XX 25-AUG-1999; 99US-00380137.
 XX 25-AUG-1999; 99US-00380138.
 XX 25-AUG-1999; 99US-00380139.
 XX 25-AUG-1999; 99US-00380142.
 XX 15-SEP-1999; 99US-00397342.
 XX 18-OCT-1999; 99US-00403297.
 XX 12-NOV-1999; 99US-00423844.
 XX 30-DEC-1999; 99WO-US031274.
 XX 18-FEB-2000; 2000WO-US004341.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 02-MAR-2000; 2000WO-US005841.
 XX 21-MAR-2000; 2000WO-US007532.
 XX 22-MAY-2000; 2000WO-US014042.
 XX 02-JUN-2000; 2000WO-US015264.
 XX 22-AUG-2000; 2000US-00544848.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 18-SEP-2000; 2000US-00664610.
 XX 18-SEP-2000; 2000US-00665350.
 XX 08-NOV-2000; 2000US-00709238.
 XX 10-NOV-2000; 2000WO-US030873.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000US-00747259.
 XX 20-DEC-2000; 2000WO-US034956.
 XX 28-FEB-2001; 2001WO-US006520.
 XX 22-MAR-2001; 2001US-00816744.
 XX 10-MAY-2001; 2001US-00854208.
 XX 10-MAY-2001; 2001US-00854280.
 XX 30-MAY-2001; 2001US-00870574.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 05-JUN-2001; 2001US-00874503.
 XX 29-JUN-2001; 2001US-00869599.
 XX 18-JUL-2001; 2001US-00908827.
 XX 06-DEC-2001; 2001US-00006867.
 PA (GETH) GENENTECH INC.
 XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-447383/42.
 XX P-PSDB; ABO27343.
 XX New isolated antibody specifically binding a PRO polypeptide, useful for
 XX the preparation of a medicament for treating disorders with the aberrant
 XX expression or activity of the PRO polypeptide, such as tumor conditions
 XX and cancer.
 XX
 XX Disclosure; Fig 125; 223pp; English.
 XX
 XX The invention relates to an antibody that binds to a secreted and
 XX transmembrane PRO polypeptide. The methods and compositions of the
 XX present invention are useful for the preparation of a medicament for the
 XX treatment of disorders associated with the aberrant expression or
 XX activity of the PRO polypeptide, such as tumour conditions and cancer.

CC They can also be used to generate transgenic or knockout animals useful
 CC in the development and screening of therapeutically useful reagents. The
 CC PRO polypeptides and encoding nucleic acids can be used as molecular
 CC weight markers for protein electrophoresis, chromosome identification and
 CC tissue typing. The antibodies may be used in various diagnostic,
 CC competitive binding and/or immunoprecipitation assays. The present
 CC sequence represents a secreted and transmembrane PRO polypeptide cDNA
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;
 Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 CCCTTATCGTCTTGGCTACTGCTGAATGTCCTCCGGAGAGGAGGAGGCTTTTGC 73
 DB 1 CCCTTATCGTCTTGGCTACTGCTGAATGTCCTCCGGAGAGGAGGAGGCTTTTGC 60
 QY 74 CGCTGACCCAGAGATGSCCCGAGCGAGCAAAATTCCTACTGTCGGCTGCGGCTACCG 133
 DB 61 CGCTGACCCAGAGATGSCCCGAGCGAGCAAAATTCCTACTGTCGGCTGCGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 193
 DB 121 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 180
 QY 194 AGCAGCTCTTGTCTGGTGGGAGCGGTGCAAGAGAAATCGCCCTATAGGGGAATGG 253
 DB 181 AGCAGCTCTTGTCTGGTGGGAGCGGTGCAAGAGAAATCGCCCTATAGGGGAATGG 240
 QY 254 TGGCCAGCGCTAGGAGGATCATGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 313
 DB 241 TGGCCAGCGCTAGGAGGATCATGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
 QY 314 CACCCGCCATTTACAGACACGTAAGTATTTGGAGGTGCAATGGTCAATATGAACATC 373
 DB 301 CACCCGCCATTTACAGACACGTAAGTATTTGGAGGTGCAATGGTCAATATGAACATC 360
 QY 374 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 433
 DB 361 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 420
 QY 434 TTGGAGGATGATGGTGTGTTATTTGGCCAGTTTTAGCCAAATCAACTGACCTAGTGA 493
 DB 421 TTGGAGGATGATGGTGTGTTATTTGGCCAGTTTTAGCCAAATCAACTGACCTAGTGA 480
 QY 494 AGTTTCAGATGCAATGGAAGGAAAGAAACTGGAAGGAAACCAATTCGGATTCGTG 553
 DB 481 AGTTTCAGATGCAATGGAAGGAAAGAAACTGGAAGGAAACCAATTCGGATTCGTG 540
 QY 554 GTGTACATCATGCTTTGCAAAAATCTTAGCTGAGGAGGAATACGAGGCTTTGGGCGAG 613
 DB 541 GTGTACATCATGCTTTGCAAAAATCTTAGCTGAGGAGGAATACGAGGCTTTGGGCGAG 600
 QY 614 GCTGGGTACCCAAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCATTTATG 673
 DB 601 GCTGGGTACCCAAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCATTTATG 660
 QY 674 ATACAGTGAACACACTCTTGGTATTTGAATACACCACTTGGAGCAATATCATGACTCAGG 733
 DB 661 ATACAGTGAACACACTCTTGGTATTTGAATACACCACTTGGAGCAATATCATGACTCAGG 720
 QY 734 GTTTTCAAGTTTATGTTCTGACCTGGTGTCTTATTTCTGGGAAACACGAGCGGATGTC 793
 DB 721 GTTTTCAAGTTTATGTTCTGACCTGGTGTCTTATTTCTGGGAAACACGAGCGGATGTC 780
 QY 794 TCAAAAGCAGAATAATGAATCAACCAAGAGATTAACAGGAAGGGAGCTTTTGTATAAAT 853
 DB 781 TCAAAAGCAGAATAATGAATCAACCAAGAGATTAACAGGAAGGGAGCTTTTGTATAAAT 840
 QY 854 CATCGACTGACCTGCTTGAATTCAGGCTGTTCAAGGTGAAGGATTCATGACTCTATATAAG 913
 DB 841 CATCGACTGACCTGCTTGAATTCAGGCTGTTCAAGGTGAAGGATTCATGACTCTATATAAG 900

Db 481 AGTTTCAGATGCAATGGAAGGAAAGAAAGCAATTCGATTCGTG 540
 QY 554 GTGTACATCATGCTTTCAGAAATCTTACGTGAGAGGAGGAATACAGAGGCTTTGGGAG 613
 Db 541 GTGTACATCATGCTTTCAGAAATCTTACGTGAGAGGAGGAATACAGAGGCTTTGGGAG 600
 QY 614 GCTGGGTACCCCAATATACAAAGAGAGCACTGCTGAAATATGGAGATTTAACCCTTATG 673
 Db 601 GCTGGGTACCCCAATATACAAAGAGAGCACTGCTGAAATATGGAGATTTAACCCTTATG 660
 QY 674 ATACAGTGAACACTACTTGTGATTTGAATACACCACTTGGAGCAATATCATGACTCAG 733
 Db 661 ATACAGTGAACACTACTTGTGATTTGAATACACCACTTGGAGCAATATCATGACTCAG 720
 QY 734 GTTTATCAAGTTTATGTTCTGCACTGCTAGCTTCTTATCTGGGAACACAGCCGATGTC 793
 Db 721 GTTTATCAAGTTTATGTTCTGCACTGCTAGCTTCTTATCTGGGAACACAGCCGATGTC 780
 QY 794 TCAAAAGCAGAAATATGAATCAACACAGAGATAAACAGAGGAGGACTTTTGTATTAAT 853
 Db 781 TCAAAAGCAGAAATATGAATCAACACAGAGATAAACAGAGGAGGACTTTTGTATTAAT 840
 QY 854 CATCACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 913
 Db 841 CATCACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 900
 QY 914 GCTTTTACCCTTGGCTGAGATGACCCCTTGGTCAATGCTTCTGGCTTACTTATG 973
 Db 901 GCTTTTACCCTTGGCTGAGATGACCCCTTGGTCAATGCTTCTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCCATTTAA 1011
 Db 961 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCCATTTAA 998

RESULT 14
 ACA67333
 ID ACA67333 standard; cDNA; 998 BP.
 AC ACA67333;
 XX
 XX
 DT 23-JUN-2003 (first entry)
 XX
 XX
 DE cDNA encoding human secreted polypeptide PRO1566.
 KW Human; Gene; ss; affinity purification.
 XX
 OS Homo sapiens.
 XX
 XX US2003027212-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 02-MAY-2002; 2002US-00063544.
 XX
 PR 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00815744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00008867.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Filvaroff B, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-341840/32.
 DR P-PSDB; AB081208.
 XX
 PT New monoclonal antibody that binds to a secreted and transmembrane
 PT polypeptide, useful for detecting and purifying the polypeptide and also
 for treating conditions responsive to the antibody.
 XX
 PS Example 4; Fig 125; 235pp; English.
 XX
 CC The invention relates to an antibody that binds to a secreted and
 CC transmembrane polypeptide, PRO1136. The antibody is useful for preparing
 CC a medicament useful in the treatment of a condition responsive to anti-
 CC PRO antibody. The antibody is also useful in diagnostic assays for PRO,
 CC by detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. The present sequence represents a cDNA encoding a PRO
 CC polypeptide of the invention
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 CCGTTATCGTCTTGCGTACTGCTGAATGTCGTCGCGGAGGAGGAGGAGGCTTTTGC 73
 Db 1 CCGTTATCGTCTTGCGTACTGCTGAATGTCGTCGCGGAGGAGGAGGAGGCTTTTGC 60
 QY 74 CGCTGACCCAGAGATGGCCCGGAGGAGCAAAATTCCTACTGTCGGCTGCGGCTACCG 133
 Db 61 CGCTGACCCAGAGATGGCCCGGAGGAGCAAAATTCCTACTGTCGGCTGCGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAGAAAACCTGACTCCAAATGCAAGAG 193
 Db 121 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAGAAAACCTGACTCCAAATGCAAGAG 180
 QY 194 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAAGAGATCTGCCCTTATAGGGGAATGG 253
 Db 181 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAAGAGATCTGCCCTTATAGGGGAATGG 240
 QY 254 TGGCAGACGCCCTTAGGATCATTTGAAGAGAGGAGCTTTCTAAAGCTTTGGCAAGAGTGA 313
 Db 241 TGGCAGACGCCCTTAGGATCATTTGAAGAGAGGAGCTTTCTAAAGCTTTGGCAAGAGTGA 300
 QY 314 CACCGCCATTATACAGACAGCTAGTGTATTTCTGGAGTCCGAATGGTCCACATATGAACATC 373
 Db 301 CACCGCCATTATACAGACAGCTAGTGTATTTCTGGAGTCCGAATGGTCCACATATGAACATC 360

QY 374 TCCGAGAGGTTGTTGGTGGCAAAAGTCAAGATGAGCAATTATCCCTTTTGGAAATCAGTCA 433
DB 361 TCCGAGAGGTTGTTGGTGGCAAAAGTCAAGATGAGCAATTATCCCTTTTGGAAATCAGTCA 420
QY 434 TTGGAGGATGATGGCTGGTGGTATTGGCCAGTATTTAGGCAATCCAACTGACCTAGTGA 493
DB 421 TTGGAGGATGATGGCTGGTGGTATTGGCCAGTATTTAGGCAATCCAACTGACCTAGTGA 480
QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAAGGAAATCTGGGAAGGAAACCAATTCGGATTTTCGTG 553
DB 481 AGGTTTCAGATGCAAAATGGAAGGAAAAGGAAATCTGGGAAGGAAACCAATTCGGATTTTCGTG 540
QY 554 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTTGGGCAG 613
DB 541 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTTGGGCAG 600
QY 614 GCTGGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
DB 601 GCTGGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660
QY 674 ATACAGTGAACACTACTCTGTTGATTAATACACCACTTGAGGACAAATATCATGACTCAG 733
DB 661 ATACAGTGAACACTACTCTGTTGATTAATACACCACTTGAGGACAAATATCATGACTCAG 720
QY 734 GTTTATCAAGTTTATGTTCTGGAAGTGGTGTAGCTTCTATTCTGGGAACACCAAGCCGATGTC 793
DB 721 GTTTATCAAGTTTATGTTCTGGAAGTGGTGTAGCTTCTATTCTGGGAACACCAAGCCGATGTC 780
QY 794 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAAGAGGGAGCTTTTGTATAAT 853
DB 781 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAAGAGGGAGCTTTTGTATAAT 840
QY 854 CATCGACTGACTGCTGATTCAGCTGTTCAAGTGGAAGATTCATGAGTCTATATAAG 913
DB 841 CATCGACTGACTGCTGATTCAGCTGTTCAAGTGGAAGATTCATGAGTCTATATAAG 900
QY 914 GCTTTTATACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
DB 901 GCTTTTATACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
QY 974 AAAAAATCAGAGATGAGTGGAGTCACTGCTTTTAA 1011
DB 961 AAAAAATCAGAGATGAGTGGAGTCACTGCTTTTAA 998

RESULT 15

ACH66306
XX ACH66306 standard; cDNA; 998 BP.
XX ACH66306;
XX ACH66306;
DT 14-OCT-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO1566 cDNA.
XX Human; secreted and transmembrane protein; PRO; gene; ss.
XX Homo sapiens.
XX
XX US2003027986-A1.
XX
XX 06-FEB-2003.
XX
XX 02-MAY-2002; 2002US-00063549.
XX
XX 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US0005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 30-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001US-00870574.
PR 05-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001US-00874503.
PR 18-JUL-2001; 2001US-00869599.
PR 06-DEC-2001; 2001US-00908827.
PR
XX
XX (GETH) GENENTECH INC.
XX
XX Baton DL, Filyaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-456358/43.
XX P-PSDB; AB053322.
XX
XX PRO polypeptide, useful for preparing a medicament for treating a
XX condition associated with PRO polypeptide.
XX
XX Disclosure; Fig 125; 222pp; English.
XX
XX The invention describes an isolated polypeptide having at least 80, 85,
XX 90, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or
XX its extracellular domain; (b) a sequence having 46-335 amino acids,
XX lacking its associated signal peptide; or (c) an amino acid sequence
XX encoded by the full-length coding sequence of the cDNA (ATCC accession
XX number 209956). The PRO (secreted and transmembrane) polypeptide is
XX useful for preparing a medicament for treating a condition associated
XX with PRO polypeptide. This sequence encodes a novel human secreted and
XX transmembrane PRO polypeptide
XX
XX SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 CCGTTATCGTCTTGGCGCTACTGCTGAATGTCGTCGCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTTATCGTCTTGGCGCTACTGCTGAATGTCGTCGCCGAGGAGGAGGAGGCTTTTGC 60
QY 74 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCCGCTGCGCGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCCGCTGCGCGCTACCG 120
QY 134 TGGCCGAGCTAGCAACTTTTCCCTCGATCTCACAATAAATCGACTCCAAATCAAGGAG 193
DB 121 TGGCCGAGCTAGCAACTTTTCCCTCGATCTCACAATAAATCGACTCCAAATCAAGGAG 180
QY 194 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGATCTGCCCTTATAGGGAATGG 253

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 04:11:05 ; Search time 105 Seconds
(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267.2	25.7	1696	4	US-09-833-381-806
2	93.4	9.0	876	4	US-09-501-558-1
3	79.6	7.7	936	4	US-09-743-847-1
4	78.4	7.5	1674	4	US-09-482-273-26
5	57.2	5.5	924	4	US-09-023-655-890
6	56.2	5.4	882	4	US-09-501-558-3
7	52.6	5.1	1430	4	US-09-489-847-39
8	50.8	4.9	1949	2	US-08-937-466-3
9	50.8	4.9	1949	3	US-09-172-528-3
10	50.8	4.9	1949	3	US-09-318-199-3
11	50.8	4.9	1949	3	US-09-503-579-3
12	49.4	4.8	930	4	US-10-001-051B-1
13	49.4	4.8	1255	1	US-08-518-878B-38
14	49.4	4.8	1255	1	US-08-294-522B-38
15	49.4	4.8	1255	1	US-08-470-868A-38
16	49.4	4.8	1596	2	US-08-807-861A-38
17	49.4	4.8	1596	2	US-09-210-681-38
18	49.4	4.8	1596	3	US-08-946-719A-38
19	49.4	4.8	1596	4	US-09-547-983-38
20	49.2	4.7	2782	2	US-08-937-466-1
21	49.2	4.7	2782	2	US-09-172-528-1
22	49.2	4.7	2782	2	US-09-318-199-1
23	49.2	4.7	2782	2	US-09-503-579-1
24	48.6	4.7	1777	2	US-08-937-466-5
25	48.6	4.7	1777	2	US-09-172-528-5
26	48.6	4.7	1777	3	US-09-318-199-5
27	48.6	4.7	1777	3	US-09-503-579-5

C	28	45.4	4.4	7218	1	US-08-232-463-14	Sequence 14, Appl
C	29	45	4.3	472	4	US-09-833-381-203	Sequence 203, App
C	30	37	3.6	1132	4	US-09-808-457-3	Sequence 3, Appli
C	31	37	3.6	1132	4	US-09-423-410-5	Sequence 5, Appli
C	32	37	3.6	1192	3	US-09-142-565-1	Sequence 1, Appli
C	33	37	3.6	1231	4	US-09-808-457-1	Sequence 3, Appli
C	34	37	3.6	1231	4	US-09-423-410-3	Sequence 3, Appli
C	35	35.2	3.4	62909	4	US-09-596-002-32	Sequence 519, App
C	36	34.2	3.3	3122	4	US-08-956-171B-519	Sequence 13438, A
C	37	34	3.3	588	4	US-09-252-991A-13438	Sequence 13803, A
C	38	34	3.3	722	4	US-09-252-991A-13803	Sequence 13909, A
C	39	34	3.3	789	4	US-08-518-878B-36	Sequence 37, Appl
C	40	34	3.3	1205	1	US-08-294-522B-37	Sequence 36, Appl
C	41	34	3.3	1205	2	US-08-807-861A-36	Sequence 36, Appl
C	42	34	3.3	1205	2	US-08-470-868A-36	Sequence 36, Appl
C	43	34	3.3	1205	2	US-09-210-681-36	Sequence 36, Appl
C	44	34	3.3	1205	3	US-08-946-719A-36	Sequence 36, Appl
C	45	34	3.3	1205	3	US-08-946-719A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-833-381-806
; Sequence 806, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-1119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-806

Query Match 25.7%; Score 267.2; DB 4; Length 1696;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 269; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	332	ACGTAGTGTATTCTTGAGGTGCGAATGGTCACATATGAAACATCTCCGAGAGGTTGTGTTTG	391
DB	1425	ACCCACTGTATTCTGGAGGTGCGAATGGTCACATATGAAACATCTCCGAGAGGTTGTGTTTG	1484
QY	392	GC AAAAGTCAGATGAGCATATCCCTTTGGAAATCAGTCATTGGAGGGATGATGCGTG	451
DB	1485	GC AAAAGTCAGATGAGCATATCCCTTTGGAAATCAGTCATTGGAGGGATGATGCGTG	1544
QY	452	GTGTTATTGGCCAGTTTGTAGCCAAATCCAACTAGTGAAGTTTCAGATCAAAATGG	511
DB	1545	GTGTTATTGGCCAGTTTGTAGCCAAATCCAACTAGTGAAGTTTCAGATCAAAATGG	1604
QY	512	AAGGAAAAAGGAAACTGGAAGGAAAAACCATTCGATTTTCGTGTGTACATCATGCAATTTG	571
DB	1605	AAGGAAAAAGGAAACTGGAAGGAAAAACCATTCGATTTTCGTGTGTACATCATGCAATTTG	1664
QY	572	CAAAAATCTTAGCTGAAGGAGGATACGAGGG	603
DB	1665	CAAAAATCTTAGCTGAAGGAGGATACGAGGG	1696

RESULT 2
US-09-501-558-1
; Sequence 1, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:

4


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; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 890:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1155218
; US-09-023-655-890

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Query Match      5.5%; Score 57.2; DB 4; Length 924;
Best Local Similarity 47.7%; Pred. No. 2.9e-09;
Matches 167; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 489 AGTGAAGGTTCCAGATGCAATTTGCAAAATGGAAGGAAAGGAAATCGAAGGAAACCATTCGCGATT 548
Db 402 AGAGGTCGTGAAAGTCAGACTTCAAGCACAGAGCCATCTCCACGGAATCAAAACCTCGCTA 461
Qy 549 TCGTGGTGTACATCATCATCTTGGCAAAATCTTAGCTGAGGAGGATACGAGGCTTTG 608
Db 462 CACGGGACTTATTAATGCGTACAGAAATAGCAACCAACGAGGCTTGACGGGCTTTG 521
Qy 609 GGCAGGCTGGGTACCCCAATATACAAAGCAGCAGCTGGTGAATATGGGAGATTAAACCA 668
Db 522 GAAAGGACTACTCCCAATCTGATGAGAGTGTCATCATCAATGTACAGAGCTAGTAAC 591
Qy 669 TTATGATACAGTGAACACTACTTTGGTATTGAATACACCACTTGAGGACAAATATCATGAC 728
Db 582 ATATGATCTAATGAAGAGGCTTTGTGAAACCAACATATTAGCAGATGACGCTCCCGTG 641
Qy 729 TCAGGTTTATCAAGTTTATGTTCTGCTGACTGGTAGCTTCTATCTGGAACACAGCCGA 788
Db 642 CCATGGTGTGGCTCTTATGCTGCTGATTTTGGCAACAGCTATGTCCTCCCGGTGGA 701
Qy 789 TGTATCAAAAGCAGAAATATGAATCAACCAAGCAGATATAACAAAGGAGGG 838
Db 702 TGTAGTAAACAGATTATTAATTTCCACCAAGCAGATACAAAGTG 751

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RESULT 6
US-09-501-558-3
; Sequence 3, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/501,558
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-09-501-558-3
Query Match      5.4%; Score 56.2; DB 4; Length 882;
Best Local Similarity 46.9%; Pred. No. 6.3e-09;
Matches 353; Conservative 0; Mismatches 358; Indels 42; Gaps 4;

Qy 124 GCGGCTACCGTGGCGGAGCTAGCAACCTTTCCCTCGATCTCACAAAATCTCGACTCCAA 183
Db 43 GCCTCCATCACTGCTGAGTGGGTACATTTCCAAATTAATTAACCAAGACACGGCTCCAG 102
Qy 184 ATCAAGAGGAGAGCAGCTCTTCTCGGTGGGAGACGCTGCAAGAGAATCTGCCCCCTAT 243
Db 103 ATTCAAGGCCAGAGATGATGCAAAATTTAAGGAAATTAGA-----TAC 147
Qy 244 AGGGGAATGTGCGCACAGCCCTTAGGATCAITTTGAAGAGGAGGCTTTCTTAAGACTTTGG 303
Db 148 CGAGGAATGTTGCACGCAITTAGTGAGTAGGACAGAGAGAGGCTGAAAGCACTCTAC 207
Qy 304 CAAGGAGTGACACCGCCCATTTTACAGACAGTAGTGTATTTCTGGAGGTGCAATGGTCACA 363
Db 208 TCGGGGATTTGCCCCCGGATTTTACCGCAGGATCTCTATGGCACCATCAAGATAGGCACT 267
Qy 364 TATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTGG 423
Db 268 TACCAGAGCTTGAAGCGACTATTTCATTGAACGCCAGAGATG-----AACTCTACCG 321
Qy 424 AATCAAGTCAATTTGAGGAGATGATGGCTGTGTTTATTTGGCCAGTTTTTTAGCCAAATCCA 483
Db 322 ATAAATGTGATATGTGGAATTTCTGTCTGGAGTCATATCTTCAACCATTTGCTAATCCA 381
Qy 484 GACCTAGTGAAGGTTCCAGATGCAAAATGGAAGGAAAGGAAACTGGAAGGAAACCACTTG 543
Db 382 GATGTTTTGAAATTCGATGCAAGCGCAAGCAACCACTTCAAGAGGAA-----433
Qy 544 CGATTTCTGGTGTATCATCATCATGCAITTTGCAAAATCTTAGCTGAAGAGGAAATACGAGG 603
Db 434 -----TGATAGGCAACTTCATG-----AACATTTACAGCAAGAGGGCAAGAGGA 480
Qy 604 CTTTGGGAGGCTGGGTACCCCAATATACAAAGAGCAGACTGGTGAATATGGAGATTTTA 663
Db 481 CTGTGAAAGGCTGTGTCCTTACTGCGCAGAGGCTGCTATTGTTGTTGTTGGTGTGGAGCTG 540
Qy 664 ACCACTTATGATACAGTGAAACACTACTTGTGTTTGAATACACCACTTGAGGACAAATATC 723
Db 541 CCGGCTATGACATCACCAAGAGCATCTTATTTCTCAGGCCCTGATGGAGACACTGTG 600
Qy 724 ATGACTCACGGTTTATCAAGTTTATGTTCTGGAAGTGTAGCTTTCTATTTCTGGGAACACCA 783
Db 601 TATACCACTTCTCTCAAGCTTCACTGTGTTGCTGGCAGGGGCCCTGGCCCTCAAAACCT 660
Qy 784 GCGGATGTCATCAAAAGCAGATATGATCAACCAAGAGATATAACCAAGAGGAGGACTTT 843
Db 661 GTTGATGTTGTGAGGACACGATGATGAATCAGAGAGTCTTTCGAGATGCGCAGATGTTCT 720
Qy 844 TTGTATAAATCATCGACTCACTGCTTGTGATTTCAG 876
Db 721 GGCTACAGGAAACCTCGATTGCTTTGTACAG 753

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RESULT 7
US-09-489-847-39
; Sequence 39, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30

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EARLIER APPLICATION NUMBER: 60/095,486
 EARLIER FILING DATE: 1998-08-05
 EARLIER APPLICATION NUMBER: 60/096,319
 EARLIER FILING DATE: 1998-08-12
 EARLIER APPLICATION NUMBER: 60/095,454
 EARLIER FILING DATE: 1998-08-06
 EARLIER APPLICATION NUMBER: 60/095,455
 EARLIER FILING DATE: 1998-08-06
 NUMBER OF SEQ ID NOS: 376
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 39
 LENGTH: 1430
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-489-847-39

Query Match 5.1%; Score 52.6; DB 4; Length 1430;
 Best Local Similarity 50.1%; Pred. No. 1.6e-07;
 Matches 201; Conservative 0; Mismatches 179; Indels 21; Gaps 2;
 QY 117 CGGCTGCGCGCTACCGTGGCGGAGCTAGCAACCTTTCCCTCGATCTCAAAAACCTCG 176
 DB 328 CGGCTTGCCTCTATCTGTGCTGAGTTGGACTTTCCCTGTGGACCTTACCAAAACAG 387
 QY 177 ACTCCAAATCAAGGAAGACAGCTCTTGTCTCGGTTGGGAGCGGTGCAAGAGAATCTGC 236
 DB 388 ACTTCAGGTTCAAGGCCAAAGCATTGATGCCGTTTCAAAGAGATAAAA----- 436
 QY 237 CCCTATAGGGATGTTGGCGGACAGCCCTAGGATCAITGAAGAGGAAGCTTCTAAA 296
 DB 437 ----TATAGAGGATGTTCCATCGCTGTTTCCATCTGTAAGAGGAAGGTTATTTGGC 492
 QY 297 GCTTTGGCAAGGAGTAGACACCCGCCATTACAGACAGTAGTGTATTCTGGAGGTGAAT 356
 DB 493 TCTCTATTAGGAATGCTCTCTGCTGTTGCTAGCAAGCATATATGGACCAATTAAT 552
 QY 357 GGTCAATATGAATCTCCGAGAGGTTGTTTGGCAAAAGTGAAGATGAGCATATATCC 416
 DB 553 TGGGATTTACAAAGCTTGAAGCGCTTATTCTGTAGAACGTTTAGAAGATGAAACT----- 607
 QY 417 CTTTGGMAATCAGTCAATTGGAGGATGATGGCTGTTGTTATTTGGCCAGTTTTTAGCCAA 476
 DB 608 -CTTTTAAATTAATGATCTGTGGGGTAGTGTGAGGAGTGATATCTTCCACTATAGCCAA 666
 QY 477 TCCAACTGACCTAGTGAAGGTTTCAGATGCAAAATGGAAGGAA 517
 DB 667 TCCACCGATGTTCTAAGATTTCATGTCAGGCTCAGGAA 707

RESULT 8
 US-08-937-466-3
 ; Sequence 3, Application US/08937466
 ; Patent No. 5846779
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Ning
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Chen, Jin-Long
 ; TITLE OF INVENTION: UCP3 Genes
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 75 DENISE DRIVE
 ; CITY: HILLSBOROUGH
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,466

FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1949 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-937-466-3
 Query Match 4.9%; Score 50.8; DB 2; Length 1949;
 Best Local Similarity 47.6%; Pred. No. 8.6e-07;
 Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;
 QY 563 ATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATACAGGGCTTTGGGAGGCTGGGTAC 622
 DB 718 ATGCCTACAGAACCATCGCCAGGGAGGAAGAGTCAAGGGCCCTGTGGAAAAGGACTTTGGC 777
 QY 623 CCAATATACAAAGAGCAGCAGCTGTTGAATATGGAGATTAAACACCTTATGATACAGTGA 682
 DB 778 CCAACATACAGAAATGCCATTTGCTCACTGCTGAGATGGTGACCTACGACATCATCA 837
 QY 683 AACACTACTTGTGTTGAATACACCACTTTGAGGACAAATATCATGACTCACGGTTTATCAA 742
 DB 838 AGGAGAAGTTGCTGGAGTCTCACCTGTTTACTGACAACTTCCCTGTCACCTTTGCTCTG 897
 QY 743 GTTTATGTTCTGACTGTTGAGTCTTCTATCTTGGGAACACAGCGGATGTCATCAAAAGCA 802
 DB 898 CTTTGGAGCTGCTTCTGTGCCACAGTGTGTGGCTCCCGGGTGGATGTGTTAAAGACC 957
 QY 803 GAATAATGAATCAACACGAGATAAACAAGGAAGGGAGCTTTTGTATATAATCATCGACTG 862
 DB 958 GATACATGAACGCTCCCTTAGGAGGTACCGCAGCCCTCTGC----- 999
 QY 863 ACTGCTTGAATCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATATAAAGGCTTTTAC 922
 DB 1000 ACTGTATGCTGAAGATGTTGGCTCAGGAGGGACCCACGGCTTCTACAAAGGATTTGTGC 1059
 QY 923 CATCTTGGCTGAGAATGACCCCTTGGTCAATGTGTCTTGGCTTACTTATGAAAAATCA 982
 DB 1060 CCTCCTTTCTGCGTCTGGGAGCTTGGAACTGTATGATGTTTGTAAACATATGAGCACTGA 1119

RESULT 9
 US-09-172-528-3
 ; Sequence 3, Application US/09172528
 ; Patent No. 5952469
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Ning
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Chen, Jin-Long
 ; TITLE OF INVENTION: UCP3 Genes
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 75 DENISE DRIVE
 ; CITY: HILLSBOROUGH
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,528
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,466
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
US-09-172-528-3

Query Match 4.9%; Score 50.8; DB 2; Length 1949;
Best Local Similarity 47.6%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;

QY 563 ATGCATTTGCAAAATCTTAGCTGAGGAGGAATACGAGGCTTTGGCAGGCTGGGTAC 622
Db 718 ATGCCTACAGAACCCAGGAGGAGGAGTACGAGGCTTTGGGAGGAGGACTTTGGC 777
QY 623 CCAATATACAAAGAGCAGCACTGGTGAATATGGAGATTTAACCACTTTATGATACAGTGA 682
Db 778 CCAACATCACAGAAATGCCATTTGCTGAGATGGTACCTACGACATCATCA 837
QY 683 AACACTACTTGGTATTTGAATACACCTTGAGGACAATATCATGACTCACGGTTTATCAA 742
Db 838 AGGAGAAGTCTGTGGAGTCTCACCTGTTTACTGACAACTTCCCTGTCCTG 897
QY 743 GTTTATGTTCTGGACTGCTTCTATTCGCGAACACAGGAGGAGTCTTGTATAAATCATCGACTG 862
Db 898 CCTTGGAGCTGGCTTCTGTGCCACAGTGGTGGCTCCCGGTGGATGTGTAAGACCC 957
QY 803 GAATAATGAATCAACACGAGATAAACAAGGAGGAGCTTTTGTATAAATCATCGACTG 862
Db 958 GATACATGAACGCTCCCTAGGAGGAGTACCGAGCCCTCTGC----- 999
QY 863 ACTGCTTGATTCAGGCTGTTCAAGGTGAAGATTCATGATCTATATAAAGGCTTTTAC 922
Db 1000 ACTGATGCTGAAGATGGTGGCTCAGGAGGAGCCACAGGCTTCTACAAAGGATTTGTGC 1059
QY 923 CATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATGAAATAATCA 982
Db 1060 CCTCTTCTGCTGGAGCTTGGAACTGATGATGTTGTAAACATATGAGCAACTGA 1119

RESULT 10
US-09-318-199-3
; Sequence 3, Application US/09318199
; Patent No. 6025469
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ning
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Chen, Jin-Long
; TITLE OF INVENTION: UCP3 Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
```

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;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/318,199
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,466
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
US-09-318-199-3

Query Match 4.9%; Score 50.8; DB 3; Length 1949;
Best Local Similarity 47.6%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;

QY 563 ATGCATTTGCAAAATCTTAGCTGAGGAGGAATACGAGGCTTTGGCAGGCTGGGTAC 622
Db 718 ATGCCTACAGAACCCAGGAGGAGGAGTACGAGGCTTTGGGAGGAGGACTTTGGC 777
QY 623 CCAATATACAAAGAGCAGCACTGGTGAATATGGAGATTTAACCACTTTATGATACAGTGA 682
Db 778 CCAACATCACAGAAATGCCATTTGCTGAGATGGTACCTACGACATCATCA 837
QY 683 AACACTACTTGGTATTTGAATACACCACTTTGAGGACAATATCATGACTCACGGTTTATCAA 742
Db 838 AGGAGAAGTCTGTGGAGTCTCACCTGTTTACTGACAACTTCCCTGTCCTG 897
QY 743 GTTTATGTTCTGGACTGTTCTATTCGCGAACACAGGAGGAGTCTTGTATAAATCATCGACTG 862
Db 898 CCTTGGAGCTGGCTTCTGTGCCACAGTGGTGGCTCCCGGTGGATGTGTAAGACCC 957
QY 803 GAATAATGAATCAACACGAGATAAACAAGGAGGAGCTTTTGTATAAATCATCGACTG 862
Db 958 GATACATGAACGCTCCCTAGGAGGAGTACCGAGCCCTCTGC----- 999
QY 863 ACTGCTTGATTCAGGCTGTTCAAGGTGAAGATTCATGATCTATATAAAGGCTTTTAC 922
Db 1000 ACTGATGCTGAAGATGGTGGCTCAGGAGGAGCCACAGGCTTCTACAAAGGATTTGTGC 1059
QY 923 CATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATGAAATAATCA 982
Db 1060 CCTCTTCTGCTGGAGCTTGGAACTGATGATGTTGTAAACATATGAGCAACTGA 1119

RESULT 11
US-09-503-579-3
; Sequence 3, Application US/09503579
; Patent No. 6248561
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ning
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Chen, Jin-Long
; TITLE OF INVENTION: UCP3 Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
```

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; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/503,579
; APPLICATION NUMBER: US/09/503,579
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,466
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-503-579-3

Query Match 4.8%; Score 50.8; DB 3; Length 1949;
Best Local Similarity 47.6%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;

QY 563 ATGCATTTCGAAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTGGGACGGCTGGGTAC 622
DB 718 ATGCTACAGAACCATCGCCAGGAGGAGAGTACAGGSCCTGTGGAAAGGACTTGGC 777
QY 623 CCAATATACAAAGACGACGACTGGTGAATATGGAGATTTAAACACTTATGATACAGTGA 682
DB 778 CCAACATACAGAAATGCCATTGTCAACTGTGTGATGATGGTGACCTACGACATCATCA 837
QY 683 AACACTACTTGGTATTGAATACACCACTTCAGGACATATCATGACTCAGGTTTATCAA 742
DB 838 AGGAGAAGTTCTGGAGTCTCACCTGTCTTACTGACCAACTTCCCTGTCTCTG 897
QY 743 GTTTATGTTCTGACTGGTAGCTTCTTATCTGGGAACACCCAGCCGATGTCATCAAAAGCA 802
DB 898 CTTTGGAGTGGCTTCTGTGCCACAGTGTGGCTCCCGGTGGATGGTAAAGACC 957
QY 803 GAATAATGAATCAACCAAGAGATAAACAAGGAAGGGGACTTTTGTATATAATCATCGACTG 862
DB 958 GATACATGAACGCTCCCTAGGAGGTACCGCAGCCCTCTGC----- 999
QY 863 ACTGCTTGTAGCTAGGCTTTCAGGTGAAGGATTCATGATCTATATAAGGCTTTTAC 922
DB 1000 ACTGTATGCTGAAGATGGTGGCTCAGGAGGAGCCACAGGCTTCTACAAAGGATTTGTGC 1059
QY 923 CATCTTGGCTGAGAATGACCCCTTGGTCAATGTTGTTCTGGCTTACTTATGAATAATCA 982
DB 1060 CTTCTTCTGCTCTGGGAGCTTGGACGTGATGATGTTGTAAACATATGACCAACTGA 1119

RESULT 12
US-10-001-051B-1
; Sequence 1, Application US/10001051B
; Patent No. 6670138
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Mirella
; APPLICANT: Shamloo, Mehrdad

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; APPLICANT: McFarland, K.C.
; APPLICANT: Chin, Daniel
; APPLICANT: Wieloch, Tadeusz
; APPLICANT: Melcher, Thorsten
; APPLICANT: AGY Therapeutics, Inc.
; TITLE OF INVENTION: METHODS OF DIAGNOSING , PREVENTING AND TREATING
; FILE REFERENCE: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/244,946
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Any animal
; OTHER INFORMATION: source, typically mammalian, most typically human
; US-10-001-051B-1

Query Match 4.8%; Score 49.4; DB 4; Length 930;
Best Local Similarity 49.1%; Pred. No. 1.5e-06;
Matches 199; Conservative 0; Mismatches 191; Indels 15; Gaps 2;

QY 103 AAATTCCTACTGTCGGCTGCGGCTACCGTCCGCGCGAGCTAGCAACCTTTCCCTGGAT 162
DB 46 AGTTTCCTTGGGGCTGGCAGCTGCTGCATCGCAGATCTCATCACCTTTCTCTGGAT 105
QY 163 CTCACAAAAAATCGACTCCAAATGCAAGGAGAGCAGCTCTTGTCTGGTTGGGAGACGGT 222
DB 106 ACTGCTTAAGTCCGGTTACAGATCCAGAGGAAAG-----TCAGGGGCCAGTCGC 156
QY 223 GCAAGAGAATTCGCCCTTATAGGGAATGGTCCGACAGCCCTTAGGGATCATTTGAAGAG 282
DB 157 GCTACAGCAGCGCCCGTACCGCGGTGTGATGGCACCATTCTGACCATGGTGGCTACT 216
QY 283 GAAGGCTTCTTAAGCTTTGGCAAGAGTGCACCCGCCATTTACAGACAGTAGTGTAT 342
DB 217 GAGGGCCCCGAGACCTCTACAATGGGTGTTGGCGGCTCGAGCGCCCAATAGAGCTTT 276
QY 343 TCTGGAGGTTCGAATGGTTCACATATGAACATCTCCGAGAGGTGTGTTTGGCAAAAGTGA 402
DB 277 GCCTCTGTCGGATCGGCTGTATGATTCTGTCAACA-----GTCTACACCAAGGC 330
QY 403 GATGACATATTCCTTTGGAAATCAGTCAATTTGGAGGAGATGATGGTGTATTTGGC 462
DB 331 TCTGAGCATGCCAGCATTTGGAGCGCCCTCTAGCAGGAGCAGCACCAGGTGCGCTGGCT 390
QY 463 CAGTTTTTAGCCANTCCAATGACCTAGTGAAGTTTCAGATGCAA 507
DB 391 GTGGCTGTGGCCCGACCCACGGATGTGTTAAAGGTCGGATTCCAA 435

RESULT 13
US-08-518-878B-38
; Sequence 38, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/518,878B
 FILING DATE: 23-AUG-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-036
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1255 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-518-878B-38

Query Match 4.8%; Score 49.4; DB 1; Length 1255;
 Best Local Similarity 49.1%; Pred. No. 1.9e-06;
 Matches 199; Conservative 0; Mismatches 191; Indels 15; Gaps 2;

QY 103 AAATTCCTACTGTCGGCTGCGGCTACCGTGGCCGAGTAGCAACTTTCCCTGGAT 162
 Db 16 AAGTTTCTTGGGCTGGCAGCTGCTGCATCGCAGATCTCATCACCTTTCTCTGGAT 75
 QY 163 CTCACAAAACCTCGACTCCAAATCAAGGAGAACGCTCTTGCTCGGTTGGGAGCGGT 222
 Db 76 ACTGCTAAAGTCCGGTTACAGATCCAAAGGAGAAAG-----TCAGGGGCCAGTGGCG 126
 QY 223 GCAAGAGAATCTGCCCCCTATAGGGGAATGGTGGCAGACGCCCTAGGGGATCATTTGAAGAG 282
 Db 127 GCTACAGTCAGCGCCAGTACCGGGTGTGATGGGCACCATCTTGACCATGGTGGCTACT 186
 QY 283 GAAGGCTTCTAAAGCTTTGGCAGGAGTAGCACCCGCCATTTACAGACAGTAGTGTAT 342
 Db 187 GAGGGCCCCGAGCCCTCAATGGGCTGTTGCGCGCTGCGCCGCAAAATGAGCTTT 246
 QY 343 TCTGGAGGTGGAATGTCACATATGAACATCTCCGAGAGGTGTGTTGGCAAAAGTGAA 402
 Db 247 GCCTCTCGCATCGGCTGTATGATCTGTCAACA-----GTTCTACCAAGGGC 300
 QY 403 GATGAGCATATCCCTTTGGAAATCAGTCATTTGGAGGAGATGCTGCTGTATTGGC 462
 Db 301 TCTGAGCATGCCAGCATTTGGGAGCGGCTCTAGCAGGCGACCAAGTGCCTGGCT 360
 QY 463 CAGTTTTAGCCATCCAACTGACCTAGTGAAGTTTCAGATGCAA 507
 Db 361 GTGGCTGGCCCCAGCCCGGATGTGGTAAAGTCCGATTCCAA 405

RESULT 14

US-08-294-522B-38
 Sequence 38, Application US/08294522B
 Patent No. 5741666
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 TITLE OF INVENTION: Compositions and Methods for the
 Treatment of Body Weight Disorders, Including Obesity
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10036-2711
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/294,522B
 FILING DATE: 23-AUG-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1255 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-294-522B-38

Query Match 4.8%; Score 49.4; DB 1; Length 1255;
 Best Local Similarity 49.1%; Pred. No. 1.9e-06;
 Matches 199; Conservative 0; Mismatches 191; Indels 15; Gaps 2;

QY 103 AAATTCCTACTGTCGGCTGCGGCTACCGTGGCCGAGTAGCAACTTTCCCTGGAT 162
 Db 16 AAGTTTCTTGGGCTGGCAGCTGCTGCATCGCAGATCTCATCACCTTTCTCTGGAT 75
 QY 163 CTCACAAAACCTCGACTCCAAATGCAAGGAGAACGCTCTTGCTCGGTTGGGAGCGGT 222
 Db 76 ACTGCTAAAGTCCGGTTACAGATCCAAAGGAGAAAG-----TCAGGGGCCAGTGGCG 126
 QY 223 GCAAGAGAATCTGCCCCCTATAGGGGAATGGTGGCAGACGCCCTAGGGGATCATTTGAAGAG 282
 Db 127 GCTACAGTCAGCGCCAGTACCGGGTGTGATGGGCACCATCTTGACCATGGTGGCTACT 186
 QY 283 GAAGGCTTCTAAAGCTTTGGCAGGAGTAGCACCCGCCATTTACAGACAGTAGTGTAT 342
 Db 187 GAGGGCCCCGAGCCCTCAATGGGCTGTTGCGCGCTGCGCCGCAAAATGAGCTTT 246
 QY 343 TCTGGAGGTGGAATGTCACATATGAACATCTCCGAGAGGTGTGTTGGCAAAAGTGAA 402
 Db 247 GCCTCTCGCATCGGCTGTATGATCTGTCAACA-----GTTCTACCAAGGGC 300
 QY 403 GATGAGCATATCCCTTTGGAAATCAGTCATTTGGAGGAGATGCTGCTGTATTGGC 462
 Db 301 TCTGAGCATGCCAGCATTTGGGAGCGGCTCTAGCAGGCGACCAAGTGCCTGGCT 360
 QY 463 CAGTTTTAGCCATCCAACTGACCTAGTGAAGTTTCAGATGCAA 507
 Db 361 GTGGCTGGCCCCAGCCCGGATGTGGTAAAGTCCGATTCCAA 405

RESULT 15

US-08-470-868A-38
 Sequence 38, Application US/08470868A
 Patent No. 5861485
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis C.
 TITLE OF INVENTION: Compositions and Methods for the
 Treatment of Body Weight Disorders, Including Obesity
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie and Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,868A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-0031-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-470-868A-38

Query Match      4.8%; Score 49.4; DB 2; Length 1255;
Best Local Similarity 49.1%; Pred. No. 1.9e-06;
Matches 199; Conservative 0; Mismatches 191; Indels 15; Gaps 2;

Qy      103 AAATTCTCTACTGTCCGGCTGCGCGGTACCGTGGCCGAGCTAGCAACCTTTCCCTCGAT 162
Db      16 AAGTTTCTTGGGGCTGCGACAGCTGCGTGCATCGCAGATCTCATCACCTTTCTCTCGAT 75

Qy      163 CTCACAAAACCTCGACTTCCAAATCCAGGAGAACAGAGCTTTGCTCGTTGGTGGGAGACGGT 222
Db      76 ACTGCTAAAGTCCGGTTTACAGATCCAAGGAGAAAG-----TCAGGGGCCAGTGGCGC 126

Qy      223 GCAAGAGAAATCTGCCCCCTATAGGGGAATGGTGGCGCAGAGCCCTAGGGATCATTTGAAGAG 282
Db      127 GCTACAGTCAGCGCCAGTACCGCGGTGTGATGGGCACCACTTCTGACCATTGGTCGGTACT 186

Qy      283 GAAGGCTTTCTAAAGCTTTGGCAAGAGTGCACCCGCCATTTTACAGACAGTGTGTAT 342
Db      187 GAGGGCCCCGAGCCCTCTACAATGGGTGGTTGCGCGCTGCAGCGCCAAATGAGCTTT 246

Qy      343 TCTGGAGTTCGATGGTTCATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAA 402
Db      247 GCCTCTCTCGCATCGCGCTGTATGATTTCTGTCAAAACA-----GTTCTACACCAAGGGC 300

Qy      403 GATGAGCATTTATCCCTTTGGAAATCAGTCAATTGGAGGGATGATGGCTGGTGTATTGGC 462
Db      301 TCTGAGCATGCCAGCATTTGGAGCGCGCTCTCTAGCAGGCACCAAGTGGCTCGCTGGCT 360

Qy      463 CAGTTTTTACGCAATCCAACTGACCTTAGTGAAGTTTCAGATGCAA 507
Db      361 GTGGCTGTGGCCAGGCCACGGATGGTGTAAAGTCCGATTTCCAA 405

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Query Match 96.1%; Score 998; DB 10; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312; Indels 0; Gaps 0;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCTTATCGCTTTCGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCCTTATCGCTTTCGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGCGCCCGGAGCGAGGAAATTCCTACTGTCGGCTGCGCGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCCGGAGCGAGGAAATTCCTACTGTCGGCTGCGCGCTACCG 120

QY 134 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 193
DB 121 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 180

QY 194 AAGCAGCTCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 253
DB 181 AAGCAGCTCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 254 TGCGCCAGCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 313
DB 181 AAGCAGCTCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 254 TGCGCCAGCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 313
DB 181 AAGCAGCTCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 241 TGCGCCAGCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 300
DB 314 CACCCGCCATTTACAGACAGTGTGTTCTGAGGTCGAATGGTCACATATGAACATC 373
DB 301 CACCCGCCATTTACAGACAGTGTGTTCTGAGGTCGAATGGTCACATATGAACATC 360

QY 374 TCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATATATCCCTTTGGAAATCAGTCA 433
DB 361 TCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATATATCCCTTTGGAAATCAGTCA 420

QY 434 TTGGAGGAGTGTGCTGCTGTTTATTTGGCCAGTCTTTTGGCAAAATCCTGACTAGTGA 493
DB 421 TTGGAGGAGTGTGCTGCTGTTTATTTGGCCAGTCTTTTGGCAAAATCCTGACTAGTGA 480

QY 494 AGCTTCAGATGCAAAATGGAAGGAAAGGAACTGGAGGAAACCAATTCGGATTTTCGTG 553
DB 481 AGCTTCAGATGCAAAATGGAAGGAAAGGAACTGGAGGAAACCAATTCGGATTTTCGTG 540

QY 554 GTGTACATCATGCTATTTGCAAAATCTTACGTGAAGGAGGAATACGAGGCTTTTGGGCAG 613
DB 541 GTGTACATCATGCTATTTGCAAAATCTTACGTGAAGGAGGAATACGAGGCTTTTGGGCAG 600

QY 614 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGGAGATTTTAAACCACTTATG 673
DB 601 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGGAGATTTTAAACCACTTATG 660

QY 674 ATACAGTGAACACTACTTGGTATTTGAATACCACTTGGAGCAATATCATGACTCAAG 733
DB 661 ATACAGTGAACACTACTTGGTATTTGAATACCACTTGGAGCAATATCATGACTCAAG 720

QY 734 GTTTATCAAGTTTATGTTCTGGACTGTGAGTCTTCTATTTCTGGGAAACACGAGCGGATGCA 793

DB 721 GTTTATCAAGTTTATGTTCTGGACTGTGAGTCTTCTATTTCTGGGAACACGAGCGGATGCA 780
QY 794 TCAAAAGCAGAAATAATGAATCAACACGAGATATAAACAAGGAGGAGGCTTTTGTATAAAT 853
DB 781 TCAAAAGCAGAAATAATGAATCAACACGAGATATAAACAAGGAGGAGGCTTTTGTATAAAT 840
QY 854 CATCGACTGACTGCTGCTTTCGATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATAAG 913
DB 841 CATCGACTGACTGCTGCTTTCGATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATAAG 900

QY 914 GCTTTTATACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGTTGTTCTGGCTTACTTATG 973
DB 901 GCTTTTATACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGTTGTTCTGGCTTACTTATG 960

QY 974 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 1011
DB 961 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 998

RESULT 2
US-10-015-395A-405
; Sequence 405, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P28301C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 405
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-395A-405

Query Match 96.1%; Score 998; DB 12; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCTTATCGCTTTCGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCCTTATCGCTTTCGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGCGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGCGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGCGCTACCG 120

QY 134 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 193
DB 121 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 180

QY 194 AAGCAGCTCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 253
DB 181 AAGCAGCTCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 254 TGCGCCAGCTTTCCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 313

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Db 241 TCGGCACAGCCCTAGGGATCAITTAAGAGGAGGCTTTCTAAGACTTTGGCAAGAGTGA 300
QY 314 CACCCGCCATTTACAGACACGTAGTGTATCTGGAGGTGCAATGATGTCATATGAACATC 373
Db 301 CACCCGCCATTTACAGACACGTAGTGTATCTGGAGGTGCAATGATGTCATATGAACATC 360
QY 374 TCCGAGAGGTGTGTGTTTGGCAAAAGTGAAGATGACATATCCCTTTGGAAATCAGTCA 433
Db 361 TCCGAGAGGTGTGTGTTGCAAAAGTGAAGATGACATATCCCTTTGGAAATCAGTCA 420
QY 434 TTGGAGGAGATGATGCTGGTGTATTTAGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 493
Db 421 TTGGAGGAGATGATGCTGGTGTATTTAGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 480
QY 494 AGGTTACAGATGCAATGCAAGGAAAGAAAGTGAAGGAAACCTGGAAGGAAACCTATGCGATTCGTTG 553
Db 481 AGGTTACAGATGCAATGCAAGGAAAGAAAGTGAAGGAAACCTGGAAGGAAACCTATGCGATTCGTTG 540
QY 554 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAG 600
QY 614 GCTGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660
QY 674 ATACAGTGAACACTACTTGGTATTTGAATACACACTTGGAGCAATATCATGACTCAAG 733
Db 661 ATACAGTGAACACTACTTGGTATTTGAATACACACTTGGAGCAATATCATGACTCAAG 720
QY 734 GTTTATCAAGTTTATGTTCTGCACTGGTGTATTTCTGGAACACCAAGGAGGCTTTTGTATAAAT 793
Db 721 GTTTATCAAGTTTATGTTCTGCACTGGTGTATTTCTGGAACACCAAGGAGGCTTTTGTATAAAT 780
QY 794 TCAAAAGCAGAAATTAATGAATCAACAGAGATAAACAAGGAGGCTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATTAATGAATCAACAGAGATAAACAAGGAGGCTTTTGTATAAAT 840
QY 854 CATGACTGATGCTGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 913
Db 841 CATGACTGATGCTGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 900
QY 914 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 973
Db 901 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 960
QY 974 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998

```

RESULT 3

```

US-10-063-745-125
; Sequence 125, Application US/10063745
; Publication No. US2004005841A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170

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; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-125

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```

Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTATTCGCTCTTGGCGTACTGCTGAATGTCCTGCGAGGAGGAGGAGGCTTTTGC 73
Db 1 CCGTATTCGCTCTTGGCGTACTGCTGAATGTCCTGCGAGGAGGAGGAGGCTTTTGC 60
QY 74 CGCTGACCCAGAGATGGCCCGGAGCAGCAAAATTCCTACTGTCTCGGCTGCGCGCTACCG 133
Db 61 CGCTGACCCAGAGATGGCCCGGAGCAGCAAAATTCCTACTGTCTCGGCTGCGCGCTACCG 120
QY 134 TGGCCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCGAAGGAG 193
Db 121 TGGCCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCGAAGGAG 180
QY 194 AAGCAGCTCTTGTCTCGGTTGGGAGACGCTGCAAGAGAATCTGCCCTTATAGGGGAATGG 253
Db 181 AAGCAGCTCTTGTCTCGGTTGGGAGACGCTGCAAGAGAATCTGCCCTTATAGGGGAATGG 240
QY 254 TGGCAGCAGCCCTAGGGATCAITTAAGAGGAAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 313
Db 241 TGGCAGCAGCCCTAGGGATCAITTAAGAGGAAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
QY 314 CACCCGCCATTTACAGACACGTAGTGTATTTCTGGAACACCAAGGCTTTTGTATAAAT 373
Db 301 CACCCGCCATTTACAGACACGTAGTGTATTTCTGGAACACCAAGGCTTTTGTATAAAT 360
QY 374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTTGGAAATCAGTCA 433
Db 361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTTGGAAATCAGTCA 420
QY 434 TTGGAGGAGATGATGCTGGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 493
Db 421 TTGGAGGAGATGATGCTGGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 480
QY 494 AGGTTACAGATGCAATTTGCAAAAGTGAAGGAAAGGAAACCTGGAAGGAAACCTATGCGATTCGTTG 553
Db 481 AGGTTACAGATGCAATTTGCAAAAGTGAAGGAAAGGAAACCTGGAAGGAAACCTATGCGATTCGTTG 540
QY 554 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAG 600
QY 614 GCTGGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660
QY 674 ATACAGTGAACACTACTTGGTATTTGAATACACACTTGGAGCAATATCATGACTCAG 733
Db 661 ATACAGTGAACACTACTTGGTATTTGAATACACACTTGGAGCAATATCATGACTCAG 720
QY 734 GTTTATCAAGTTTATGTTCTGCACTGGTGTATTTCTGGAACACCAAGGAGGCTTTTGTATAAAT 793
Db 721 GTTTATCAAGTTTATGTTCTGCACTGGTGTATTTCTGGAACACCAAGGAGGCTTTTGTATAAAT 780
QY 794 TCAAAAGCAGAAATTAATGAATCAACAGAGATAAACAAGGAGGCTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATTAATGAATCAACAGAGATAAACAAGGAGGCTTTTGTATAAAT 840
QY 854 CATGACTGATGCTGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 913
Db 841 CATGACTGATGCTGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 900
QY 914 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 973
Db 901 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 960

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Db 121 TGGCCGAGCTAGCAACCTTCCCTGGATCTCACAACAACTCGACTCAATGCAAGAG 180
Qy 134 AAGAGCTCTTCTCGTGGGAGACGGTCAAGAGAACTCTGCCCTTATAGGGAATGG 253
Db 181 AAGAGCTCTTCTCGTGGGAGACGGTCAAGAGAACTCTGCCCTTATAGGGAATGG 240
Qy 254 TGGCAGACAGCCTAGGGATCAATGAAGAGGAGGCTTCTAAAGCTTTGGCAAGAGTGA 313
Db 241 TGGCAGACAGCCTAGGGATCAATGAAGAGGAGGCTTCTAAAGCTTTGGCAAGAGTGA 300
Qy 314 CACCCGCCATTTACAGACACCTAGTGTATTTCTGAGGTCTGAATGCTCACAATCAACATC 373
Db 301 CACCCGCCATTTACAGACACCTAGTGTATTTCTGAGGTCTGAATGCTCACAATCAACATC 360
Qy 374 TCCGAGAGGTTGTGTTGGGAAAGTGAAGATGAGCAATTTCCCTTTGGAAATCAGTCA 433
Db 361 TCCGAGAGGTTGTGTTGGGAAAGTGAAGATGAGCAATTTCCCTTTGGAAATCAGTCA 420
Qy 434 TTGGAGGATCATGGCTGTGTTATTTGGCCAGTTTATTTAGCCAACTCCAACTGACCTAGTGA 493
Db 421 TTGGAGGATCATGGCTGTGTTATTTGGCCAGTTTATTTAGCCAACTCCAACTGACCTAGTGA 480
Qy 494 AGGTTTCAGATCAAAATGGAAGGAAAGAAAGAACTGGAAGGAAACCAATTCGGATTTCTGTG 553
Db 481 AGGTTTCAGATCAAAATGGAAGGAAAGAAAGAACTGGAAGGAAACCAATTCGGATTTCTGTG 540
Qy 554 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTGGGCAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTGGGCAG 600
Qy 614 GCTGGGTACCAATATACAAAGACGACCTGTTGTAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGGTACCAATATACAAAGACGACCTGTTGTAATATGGGAGATTTAAACCACTTATG 660
Qy 674 ATACAGTGAACACTACTTGTGTAATGTAATACCACTTTGAGGACAAATATCATGACTCAG 733
Db 661 ATACAGTGAACACTACTTGTGTAATGTAATACCACTTTGAGGACAAATATCATGACTCAG 720
Qy 734 GTTTATCAAGTTTATGTTCTGGACTGTGATTTCTTCTGGGAAACACCGCGATGTCA 793
Db 721 GTTTATCAAGTTTATGTTCTGGACTGTGATTTCTTCTGGGAAACACCGCGATGTCA 780
Qy 794 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAAAGGAAAGGAGCTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAAAGGAAAGGAGCTTTTGTATAAAT 840
Qy 854 CATGACTGACTGCTTGAATTCAGGCTGTTCAAGGTGAAGATTCATGAGTCTATATAAAG 913
Db 841 CATGACTGACTGCTTGAATTCAGGCTGTTCAAGGTGAAGATTCATGAGTCTATATAAAG 900
Qy 914 GCTTTTACCACCTTGGCTGAGATGACCTTGGTCAATGCTGTTCTGGCTTACTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGATGACCTTGGTCAATGCTGTTCTGGCTTACTATG 960
Qy 974 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998

```

RESULT 6

US-10-063-569-125
; Sequence 125, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-569-125

Query Match 96.1%; Score 998; DB 13; Length 998;

Best Local Similarity 100.0%; Pred. No. 5.3e-312;

Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 14 CCCTTATCGTCTTGGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 73
Db 1 CCCTTATCGTCTTGGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 60
Qy 74 CGCTGACCCAGAGATGGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGGGCTACCG 133
Db 61 CGCTGACCCAGAGATGGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGGGCTACCG 120
Qy 134 TGGCCGAGCTAGCAACTTTTCCCTCGATCTCACAATAACTCGACTCCAAATGCAAGGAG 193
Db 121 TGGCCGAGCTAGCAACTTTTCCCTCGATCTCACAATAACTCGACTCCAAATGCAAGGAG 180
Qy 194 AAGCAGCTCTTCTCGTGGTGGGAGCGGTGCAAGAGAAATCTCCCTTATAGGGAATGG 253
Db 181 AAGCAGCTCTTCTCGTGGTGGGAGCGGTGCAAGAGAAATCTCCCTTATAGGGAATGG 240
Qy 254 TGGCCAGCCCTTAGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTTGGCAAGAGTGA 313
Db 241 TGGCCAGCCCTTAGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTTGGCAAGAGTGA 300
Qy 314 CACCCGCCATTTACAGACACCTAGTGTATTTCTGAGGTCTGAATGCTCACAATGCAATC 373
Db 301 CACCCGCCATTTACAGACACCTAGTGTATTTCTGAGGTCTGAATGCTCACAATGCAATC 360
Qy 374 TCCGAGAGGCTTGTGTTGGCAAAAGTGAAGATGAGCAATTCCTTTCGAAATCAGTCA 433
Db 361 TCCGAGAGGCTTGTGTTGGCAAAAGTGAAGATGAGCAATTCCTTTCGAAATCAGTCA 420
Qy 434 TTGGAGGATGATGCTGCTGTTATTTGGCCAGTTTATTTAGCCAACTCCAACTGACCTAGTGA 493
Db 421 TTGGAGGATGATGCTGCTGTTATTTGGCCAGTTTATTTAGCCAACTCCAACTGACCTAGTGA 480
Qy 494 AGGTTTCAGATCAAAATGGAAGGAAAGAAAGAACTGGAAGGAAACCAATTCGGATTTCTGTG 553
Db 481 AGGTTTCAGATCAAAATGGAAGGAAAGAAAGAACTGGAAGGAAACCAATTCGGATTTCTGTG 540
Qy 554 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGGAGGAAATACAGAGGCTTTTGGGCAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGGAGGAAATACAGAGGCTTTTGGGCAG 600
Qy 614 GCTGGGTACCAATATACAAAGACGACCTGTTGTAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGGTACCAATATACAAAGACGACCTGTTGTAATATGGGAGATTTAAACCACTTATG 660
Qy 674 ATACAGTGAACACTACTTGTGTAATGTAATACCACTTTGAGGACAAATATCATGACTCAG 733
Db 661 ATACAGTGAACACTACTTGTGTAATGTAATACCACTTTGAGGACAAATATCATGACTCAG 720
Qy 734 GTTTATCAAGTTTATGTTCTGGACTGTGATTTCTTCTGGGAAACACCGCGATGTCA 793
Db 721 GTTTATCAAGTTTATGTTCTGGACTGTGATTTCTTCTGGGAAACACCGCGATGTCA 780
Qy 794 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAAAGGAAAGGAGCTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAAAGGAAAGGAGCTTTTGTATAAAT 840

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[illegible]

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; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match          96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATTCCTACTGTCGCGCTCGCGGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATTCCTACTGTCGCGCTCGCGGCTACCG 120

QY 134 TGCGCCGAGCTAGCAACTCTTCCCTCGATCTCAAAAAAATCGACTCCAAATCAAGGAG 193
DB 121 TGCGCCGAGCTAGCAACTCTTCCCTCGATCTCAAAAAAATCGACTCCAAATCAAGGAG 180

QY 194 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAAATCTGCCCCCTATAGGGGAATGG 253
DB 181 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAAATCTGCCCCCTATAGGGGAATGG 240

QY 254 TGCGCACGCCCTAGGATCATTAAGAGGAGGCTTCTTAAGCTTTGGCAAGGAGTGA 313
DB 241 TGCGCACGCCCTAGGATCATTAAGAGGAGGCTTCTTAAGCTTTGGCAAGGAGTGA 300

QY 314 CACCCGCCATTTACAGACACGTAAGTCTATTCTGGAGTGAATGGTCAATATGAACATC 373
DB 301 CACCCGCCATTTACAGACACGTAAGTCTATTCTGGAGTGAATGGTCAATATGAACATC 360

QY 374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 433
DB 361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 420

QY 434 TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 493
DB 421 TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 480

QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGAAGGAAAAACCATTTGCCATTTTCGTG 553
DB 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGAAGGAAAAACCATTTGCCATTTTCGTG 540

QY 554 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTTGGGCGAG 613
DB 541 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTTGGGCGAG 600

QY 614 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 673
DB 601 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 660

674 ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 733
661 ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 720
734 GTTTATCAAGTTTATGTTCTGGACTGCTAGCTTCTATTCTGGGAAACACCGCGGATGCA 793
721 GTTTATCAAGTTTATGTTCTGGACTGCTAGCTTCTATTCTGGGAAACACCGCGGATGCA 780
794 TCAAAAGCAGAATAATGAATCAACACGAGATAAACAGGAAGGGGACTTTTGTATATAAT 853
781 TCAAAAGCAGAATAATGAATCAACACGAGATAAACAGGAAGGGGACTTTTGTATATAAT 840
854 CATCGACTGACTGCTTGTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 913
841 CATCGACTGACTGCTTGTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 900
914 GCTTTTACCATCTTGGCTGAGNATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
901 GCTTTTACCATCTTGGCTGAGNATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
974 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCCATTTTAA 1011
961 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCCATTTTAA 998

RESULT 9
US-10-013-907A-405
; Sequence 405, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 405
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-013-907A-405

Query Match          96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATTCCTACTGTCGCGCTCGCGGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATTCCTACTGTCGCGCTCGCGGCTACCG 120

QY 134 TGCGCCGAGCTAGCAACTCTTCCCTCGATCTCAAAAAAATCGACTCCAAATCAAGGAG 193
DB 121 TGCGCCGAGCTAGCAACTCTTCCCTCGATCTCAAAAAAATCGACTCCAAATCAAGGAG 180

QY 194 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAAATCTGCCCCCTATAGGGGAATGG 253
DB 181 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAAATCTGCCCCCTATAGGGGAATGG 240

QY 254 TGCGCACGCCCTAGGATCATTAAGAGGAGGCTTCTTAAGCTTTGGCAAGGAGTGA 313
DB 241 TGCGCACGCCCTAGGATCATTAAGAGGAGGCTTCTTAAGCTTTGGCAAGGAGTGA 300

QY 314 CACCCGCCATTTACAGACACGTAAGTCTATTCTGGAGTGAATGGTCAATATGAACATC 373
DB 301 CACCCGCCATTTACAGACACGTAAGTCTATTCTGGAGTGAATGGTCAATATGAACATC 360

QY 374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 433
DB 361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 420

QY 434 TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 493
DB 421 TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 480

QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGAAGGAAAAACCATTTGCCATTTTCGTG 553
DB 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGAAGGAAAAACCATTTGCCATTTTCGTG 540

QY 554 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTTGGGCGAG 613
DB 541 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTTGGGCGAG 600

QY 614 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 673
DB 601 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 660
```

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QY 194 AAGCAGCTCTTCTCGTGGGAGACGGTCAAGAGAACTCTGCCCTATAGGGAATGG 253
Db |||
QY 198 AAGCAGCTCTTCTCGTGGGAGACGGTCAAGAGAACTCTGCCCTATAGGGAATGG 240
Db |||
QY 254 TCGGCACAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 313
Db |||
QY 241 TCGGCACAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
Db |||
QY 314 CACCGCCATTTACAGACACGCTAGTGTATTTCTGAGGTGCAATGGTGCATATGAACATC 373
Db |||
QY 301 CACCGCCATTTACAGACACGCTAGTGTATTTCTGAGGTGCAATGGTGCATATGAACATC 360
Db |||
QY 374 TCCGAGAGGTGTGTCTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 433
Db |||
QY 361 TCCGAGAGGTGTGTCTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 420
Db |||
QY 434 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTGTAGCCAAATCCAACTGACCTAGTGA 493
Db |||
QY 421 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTGTAGCCAAATCCAACTGACCTAGTGA 480
Db |||
QY 494 AGGTTTCAGATGCAATGCAAGGAAAGGAAGAACTGGAAGGAAACCAATTCGGATTCGTG 553
Db |||
QY 481 AGGTTTCAGATGCAATGCAAGGAAAGGAAGAACTGGAAGGAAACCAATTCGGATTCGTG 540
Db |||
QY 554 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATAACGAGGCTTTGGGCAG 613
Db |||
QY 541 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATAACGAGGCTTTGGGCAG 600
Db |||
QY 614 GCTGGGTACCCAAATATCAAGAGCAGCACTGTGTGAATATGGGAGATTTAAACCACTTATG 673
Db |||
QY 601 GCTGGGTACCCAAATATCAAGAGCAGCACTGTGTGAATATGGGAGATTTAAACCACTTATG 660
Db |||
QY 674 ATACAGTGAACACTACTTGTGTATTAATACACACTTGGAGGAACCAATATCATGACTCAG 733
Db |||
QY 661 ATACAGTGAACACTACTTGTGTATTAATACACACTTGGAGGAACCAATATCATGACTCAG 720
Db |||
QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTAGTCTTATTTCTGGGAACACAGCCGATGCA 793
Db |||
QY 721 GTTTATCAAGTTTATGTTCTGGACTGGTAGTCTTATTTCTGGGAACACAGCCGATGCA 780
Db |||
QY 794 TCAAAGCAGATTAATGAATCAACGAGATAAACAAGGAAGGGGACTTTTGTATATAAT 853
Db |||
QY 781 TCAAAGCAGATTAATGAATCAACGAGATAAACAAGGAAGGGGACTTTTGTATATAAT 840
Db |||
QY 854 CATCGACTGACTGCTTGTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 913
Db |||
QY 841 CATCGACTGACTGCTTGTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 900
Db |||
QY 914 GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
Db |||
QY 901 GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
Db |||
QY 974 AAAAAATCAGAGATGAGTGGAGTCACTCCATTTTAA 1011
Db |||
QY 961 AAAAAATCAGAGATGAGTGGAGTCACTCCATTTTAA 998
Db |||
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RESULT 10

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US-10-015-499A-405
; Sequence 405, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
```

```
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 405
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-499A-405
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Query Match 96.1%; Score 998; DB 13; Length 998;

Best Local Similarity 100.0%; Pred. No. 5,3e-312; Mismatches 0; Indels 0; Gaps 0;

Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 14 CCCTTATCGTCTTTCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
Db |||
QY 74 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGCGCTCGCGGCTACCG 133
Db |||
QY 61 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGCGCTCGCGGCTACCG 120
Db |||
QY 134 TGCGCAGCTAGCAACTTTTCCCTCGATCTCACAAAAAATCGACTCCAAATGCAAGGAG 193
Db |||
QY 121 TGCGCAGCTAGCAACTTTTCCCTCGATCTCACAAAAAATCGACTCCAAATGCAAGGAG 180
Db |||
QY 194 AGCAGCTCTTTCGCTGGTGGAGACGGTGAAGAGAAATTCGCCCTATAGGGAATGG 253
Db |||
QY 181 AAGCAGCTCTTTCGCTGGTGGAGACGGTGAAGAGAAATTCGCCCTATAGGGAATGG 240
Db |||
QY 254 TGCGCAGCAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTTCGCAAGGAGTGA 313
Db |||
QY 241 TGCGCAGCAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTTCGCAAGGAGTGA 300
Db |||
QY 314 CACCGCCATTTACAGACACGCTAGTGTATTTCTGAGGTGCAATGGTGCATATGAACATC 373
Db |||
QY 301 CACCGCCATTTACAGACACGCTAGTGTATTTCTGAGGTGCAATGGTGCATATGAACATC 360
Db |||
QY 374 TCGAGAGGCTGTGTTGCAAAAGTGAAGATGAGCAATATCCCTTTGGAATCAGTCA 433
Db |||
QY 361 TCGAGAGGCTGTGTTGCAAAAGTGAAGATGAGCAATATCCCTTTGGAATCAGTCA 420
Db |||
QY 434 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTGTAGCCAAATCCAACTGACCTAGTGA 493
Db |||
QY 421 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTGTAGCCAAATCCAACTGACCTAGTGA 480
Db |||
QY 494 AGGTTTCAGATGCAATGCAAGGAAAGGAAGAACTGGAAGGAAACCAATTCGGATTCGTG 553
Db |||
QY 481 AGGTTTCAGATGCAATGCAAGGAAAGGAAGAACTGGAAGGAAACCAATTCGGATTCGTG 540
Db |||
QY 554 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATAACGAGGCTTTGGGCAG 613
Db |||
QY 541 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATAACGAGGCTTTGGGCAG 600
Db |||
QY 614 GCTGGGTACCCAAATATCAAGAGCAGCACTGTGTGAATATGGGAGATTTAAACCACTTATG 673
Db |||
QY 601 GCTGGGTACCCAAATATCAAGAGCAGCACTGTGTGAATATGGGAGATTTAAACCACTTATG 660
Db |||
QY 674 ATACAGTGAACACTACTTGTGTATTAATACACACTTGGAGGAACCAATATCATGACTCAG 733
Db |||
QY 661 ATACAGTGAACACTACTTGTGTATTAATACACACTTGGAGGAACCAATATCATGACTCAG 720
Db |||
QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTAGTCTTATTTCTGGGAACACAGCCGATGCA 793
Db |||
QY 721 GTTTATCAAGTTTATGTTCTGGACTGGTAGTCTTATTTCTGGGAACACAGCCGATGCA 780
Db |||
QY 794 TCAAAGCAGATTAATGAATCAACGAGATAAACAAGGAAGGGGACTTTTGTATATAAT 853
Db |||
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QY 14 CCGTTATCGTCTTGGCTACTGCTGAATCTCCGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
 Db 1 CCGTTATCGTCTTGGCTACTGCTGAATCTCCGTCCTCCGAGGAGGAGGAGGCTTTTGC 60
 QY 74 CCGTGACCCAGAGATGGCCCGGAGGAGCAAAATCTCTACTGTCCTGGCTGCGGGCTACCG 133
 Db 61 CCGTGACCCAGAGATGGCCCGGAGGAGCAAAATCTCTACTGTCCTGGCTGCGGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAGAAAACTCGATCCAAATGCAAGGAG 193
 Db 121 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAGAAAACTCGATCCAAATGCAAGGAG 180
 QY 194 AAGCAGCTCTTCTCGTGGGAGAGCTGCAAGAGATCTCCCTTGGCAAGGAGGCTTTTGC 253
 Db 181 AAGCAGCTCTTCTCGTGGGAGAGCTGCAAGAGATCTCCCTTGGCAAGGAGGCTTTTGC 240
 QY 254 TGGCCAGCCCTAGGATCAATGAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 313
 Db 241 TGGCCAGCCCTAGGATCAATGAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
 QY 314 CACCCGCGCATTTACAGACAGCTAGTGTATCTGAGGTCGAATGGTCAATGCAATC 373
 Db 301 CACCCGCGCATTTACAGACAGCTAGTGTATCTGAGGTCGAATGGTCAATGCAATC 360
 QY 374 TCCGAGAGGCTTGTCTTGGCAAAAGTGAAGATGAGCATTTCCCTTGGCAAGGAGTGA 433
 Db 361 TCCGAGAGGCTTGTCTTGGCAAAAGTGAAGATGAGCATTTCCCTTGGCAAGGAGTGA 420
 QY 434 TGGAGGATGATGGCTGGTGTATTTGGCCAAAGTGAAGATGAGCATTTCCCTTGGCAAGGAGTGA 493
 Db 421 TGGAGGATGATGGCTGGTGTATTTGGCCAAAGTGAAGATGAGCATTTCCCTTGGCAAGGAGTGA 480
 QY 494 AGGTTTCAGATCAATGGAAGGAAAAAGGAACTGGAAGGAAAACTGGAATGCGATTTTGC 553
 Db 481 AGGTTTCAGATCAATGGAAGGAAAAAGGAACTGGAAGGAAAACTGGAATGCGATTTTGC 540
 QY 554 GTGTACATCATGCAATTTGCAAAAAATCTTAGTGAAGGAGGAAATACGAGGCTTTGGGCGAG 613
 Db 541 GTGTACATCATGCAATTTGCAAAAAATCTTAGTGAAGGAGGAAATACGAGGCTTTGGGCGAG 600
 QY 614 GCTGGGTACCCCAATATACAAAGAGCAGCAGCTGGTGAATATGGGAGATTTTAAACCATTTATG 673
 Db 601 GCTGGGTACCCCAATATACAAAGAGCAGCAGCTGGTGAATATGGGAGATTTTAAACCATTTATG 660
 QY 674 ATACAGTGAACACTACTTGGTATTTGAATACACACTTTGAGGACAAATATCATGACTCAGC 733
 Db 661 ATACAGTGAACACTACTTGGTATTTGAATACACACTTTGAGGACAAATATCATGACTCAGC 720
 QY 734 GTTTATCAAGTTTATGTTCTGGACTGTAGCTTCTATTTCTGGAAACACAGCCGATGTCA 793
 Db 721 GTTTATCAAGTTTATGTTCTGGACTGTAGCTTCTATTTCTGGAAACACAGCCGATGTCA 780
 QY 794 TCAAAAGCAGAAATGAATCAACCCAGAGATAAACAGGAGGAGCTTTGTATAAAT 853
 Db 781 TCAAAAGCAGAAATGAATCAACCCAGAGATAAACAGGAGGAGCTTTGTATAAAT 840
 QY 854 CATCGACTGCTGTTGATTCAGGCTGTTCAAGGTCGAAGATTCATGAGTCTATATAAAG 913
 Db 841 CATCGACTGCTGTTGATTCAGGCTGTTCAAGGTCGAAGATTCATGAGTCTATATAAAG 900
 QY 914 GCTTTTACCCTCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
 Db 901 GCTTTTACCCTCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011
 Db 961 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998

RESULT 13

US-10-063-594-125

; Sequence 125, Application US/10063594

Publication No. US20030065161A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,594
 CURRENT FILING DATE: 2002-05-30
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 125
 LENGTH: 998
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-063-594-125

Query Match 96.1%; Score 998; DB 13; Length 998;
 Best Local Similarity 100.0%; Pred. No. 5.3e-312;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 CCGTTATCGTCTTGGCTACTGCTGAATCTCCGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
 Db 1 CCGTTATCGTCTTGGCTACTGCTGAATCTCCGTCCTCCGAGGAGGAGGAGGCTTTTGC 60
 QY 74 CCGTGACCCAGAGATGGCCCGGAGGAGCAAAATCTCTACTGTCCTGGCTGCGGGCTACCG 133
 Db 61 CCGTGACCCAGAGATGGCCCGGAGGAGCAAAATCTCTACTGTCCTGGCTGCGGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAGAAAACTCGATCCAAATGCAAGGAG 193
 Db 121 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCAGAAAACTCGATCCAAATGCAAGGAG 180
 QY 194 AAGCAGCTCTTCTCGTGGGAGAGCTGCAAGAGATCTGCCCCCTTATGGGGAATGG 253
 Db 181 AAGCAGCTCTTCTCGTGGGAGAGCTGCAAGAGATCTGCCCCCTTATGGGGAATGG 240
 QY 254 TGGCCAGCCCTAGGATCAATGAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 313
 Db 241 TGGCCAGCCCTAGGATCAATGAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
 QY 314 CACCCGCGCATTTACAGACAGCTAGTGTATTTCTGGAGGTCGAATGCTACATATGAACATC 373
 Db 301 CACCCGCGCATTTACAGACAGCTAGTGTATTTCTGGAGGTCGAATGCTACATATGAACATC 360
 QY 374 TCCGAGAGGCTTGTCTTGGCAAAAGTGAAGATGAGCATTTCCCTTGGAAATCAGTCA 433
 Db 361 TCCGAGAGGCTTGTCTTGGCAAAAGTGAAGATGAGCATTTCCCTTGGAAATCAGTCA 420
 QY 434 TGGAGGATGATGGCTGGTGTATTTGGCCAAAGTGAAGATGAGCATTTCCCTTGGCAAGGAGTGA 493
 Db 421 TGGAGGATGATGGCTGGTGTATTTGGCCAAAGTGAAGATGAGCATTTCCCTTGGCAAGGAGTGA 480
 QY 494 AGGTTTCAGATCAATGGAAGGAAAAAGGAACTGGAAGGAAAACTGGAATGCGATTTTGC 553
 Db 481 AGGTTTCAGATCAATGGAAGGAAAAAGGAACTGGAAGGAAAACTGGAATGCGATTTTGC 540
 QY 554 GTGTACATCATGCAATTTGCAAAAAATCTTAGTGAAGGAGGAAATACGAGGCTTTGGGCGAG 613
 Db 541 GTGTACATCATGCAATTTGCAAAAAATCTTAGTGAAGGAGGAAATACGAGGCTTTGGGCGAG 600
 QY 614 GCTGGGTACCCCAATATACAAAGAGCAGCAGCTGGTGAATATGGGAGATTTTAAACCATTTATG 673
 Db 601 GCTGGGTACCCCAATATACAAAGAGCAGCAGCTGGTGAATATGGGAGATTTTAAACCATTTATG 660
 QY 674 ATACAGTGAACACTACTTGGTATTTGAATACACACTTTGAGGACAAATATCATGACTCAGC 733

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Db 661 ATACAGTGAACACTACTTGTGATTGAATACCACTTGAGGACAATATCATGACTCAG 720
Qy 734 GTTTATCAAGTTTATGTTCTGGAGTGTAGTCTTCTATCTCGGGAACACACGCGGATGTC 793
Db 721 GTTTATCAAGTTTATGTTCTGGAGTGTAGTCTTCTATCTCGGGAACACACGCGGATGTC 780
Qy 794 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAGGAAGGAGCTTTTGTATATAAT 853
Db 781 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAGGAAGGAGCTTTTGTATATAAT 840
Qy 854 CATGAGTACTGCTGTTGATTCAGGCTGTTCAAGGTGAAGATTATGAGTCTATATAAG 913
Db 841 CATGAGTACTGCTGTTGATTCAGGCTGTTCAAGGTGAAGATTATGAGTCTATATAAG 900
Qy 914 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGCTTACTTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGCTTACTTATG 960
Qy 974 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998

RESULT 14
US-10-063-553-125
; Sequence 125, Application US/10063553
; Publication No. US20030045684A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,553
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-553-125

Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312; Indels 0; Gaps 0;
Matches 998; Conservative 0; Mismatches 0;

Qy 14 CCGTTATCGTCTTCCGCTACTGCTGAATGTCCTCCGAGGAGGAGAGGCTTTTGC 73
Db 1 CCGTTATCGTCTTCCGCTACTGCTGAATGTCCTCCGAGGAGGAGAGGCTTTTGC 60
Qy 74 CGTGACCCAGAGATGGCCCGGAGCGAGCAAAATTCCTACTGTCCGCTGCGGCTACCG 133
Db 61 CGTGACCCAGAGATGGCCCGGAGCGAGCAAAATTCCTACTGTCCGCTGCGGCTACCG 120
Qy 134 TGGCCGAGCTAGCAACTTTCCTCGATCTCAAAATCTGACTCCAAATGCAAGGAG 193
Db 121 TGGCCGAGCTAGCAACTTTCCTCGATCTCAAAATCTGACTCCAAATGCAAGGAG 180
Qy 194 AAGCAGCTCTTGTCCGTTGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG 253
Db 181 AAGCAGCTCTTGTCCGTTGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG 240
Qy 254 TGGCACAAGCCCTTAGGATCATTTGAAGAGAGGCTTTCTAAAGCTTTTGGCAAGGATGA 313
```

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Db 241 TCGCACAAGCCCTTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
Qy 314 CACCCGCCATTTACAGACACAGTGTATCTGAGGTGGAATGGTGCATATGAAACATC 373
Db 301 CACCCGCCATTTACAGACACAGTGTATCTGAGGTGGAATGGTGCATATGAAACATC 360
Qy 374 TCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATTCAGTCA 433
Db 361 TCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATTCAGTCA 420
Qy 434 TCGAGGAGTGTGCTGCTGCTGTTATTTGGCCAGTTTTAGCCATCCAACTGACCTAGTGA 493
Db 421 TCGAGGAGTGTGCTGCTGCTGTTATTTGGCCAGTTTTAGCCATCCAACTGACCTAGTGA 480
Qy 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAACTCGAAGGAAAAACATTCGGAATTTTCGTG 553
Db 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAACTCGAAGGAAAAACATTCGGAATTTTCGTG 540
Qy 554 GTGTACATCATGCTTTTGC AAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTTGGGAG 613
Db 541 GTGTACATCATGCTTTTGC AAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTTGGGAG 600
Qy 614 GCTGGGTACCCATATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTTAAACCACTTATG 673
Db 601 GCTGGGTACCCATATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTTAAACCACTTATG 660
Qy 674 ATACAGTGAACACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 733
Db 661 ATACAGTGAACACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 720
Qy 734 GTTTATCAAGTTTATGTTCTGGAGTGTAGTCTTCTATCTTGGGAACACACGAGCGGATGTC 793
Db 721 GTTTATCAAGTTTATGTTCTGGAGTGTAGTCTTCTATCTTGGGAACACACGAGCGGATGTC 780
Qy 794 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAGGAGGAGCTTTTGTATATAAT 853
Db 781 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAGGAGGAGCTTTTGTATATAAT 840
Qy 854 CATGAGTACTGCTGTTGATTCAGGCTGTTCAAGGTGAAGATTATGAGTCTATATAAG 913
Db 841 CATGAGTACTGCTGTTGATTCAGGCTGTTCAAGGTGAAGATTATGAGTCTATATAAG 900
Qy 914 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGCTTACTTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGCTTACTTATG 960
Qy 974 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998
```

RESULT 15

US-10-063-554-125
; Sequence 125, Application US/10063554
; Publication No. US20030040013A1
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,554
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125

! LENGTH: 998
! TYPE: DNA
! ORGANISM: Homo Sapien
US-10-063-554-125

Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	14	CGTTATCGTCTTGGCTACTGCTGAATGTCGCTCCGAGGAGGAGGAGGCTTTTGC	73
Db	1	CGTTATCGTCTTGGCTACTGCTGAATGTCGCTCCGAGGAGGAGGAGGCTTTTGC	60
Qy	74	CGTCACCCAGAGATGGCCGAGCGAGCAAAATTCCTACTCTCCGGCTGCGGGCTACCG	133
Db	61	CGTCACCCAGAGATGGCCGAGCGAGCAAAATTCCTACTCTCCGGCTGCGGGCTACCG	120
Qy	134	TGGCCGAGCTAGCAACCTTTCCCTCGATCTCACAAAACCTCGACTCCAAATGCAAGGAG	193
Db	121	TGGCCGAGCTAGCAACCTTTCCCTCGATCTCACAAAACCTCGACTCCAAATGCAAGGAG	180
Qy	194	AAGCAGCTCTTCTCGGTTGGGAGACGTCGAGAAATCTGCCCTTATAGGGGAATGG	253
Db	181	AAGCAGCTCTTCTCGGTTGGGAGACGTCGAGAAATCTGCCCTTATAGGGGAATGG	240
Qy	254	TGCGCACAGCCCTAGGGATCAATGAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
Db	241	TGCGCACAGCCCTAGGGATCAATGAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
Qy	314	CACCGCCCATTTACAGACACACACACACACACACACACACACACACACACACATC	373
Db	301	CACCGCCCATTTACAGACACACACACACACACACACACACACACACACACACATC	360
Qy	374	TCCGAGAGGTTGCTTTGGCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	433
Db	361	TCCGAGAGGTTGCTTTGGCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	420
Qy	434	TTGAGGGAGTATGGCTGGTGTATTTGGCCAGTATTTAGCCAAATCCAACTGACCTAGTGA	493
Db	421	TTGAGGGAGTATGGCTGGTGTATTTAGCCAGTATTTAGCCAAATCCAACTGACCTAGTGA	480
Qy	494	AGTTTCAGATGCAATGGAAGGAAAGGAACTGGAAGGAAACCAATTCGGATTCGTG	553
Db	481	AGTTTCAGATGCAATGGAAGGAAAGGAACTGGAAGGAAACCAATTCGGATTCGTG	540
Qy	554	GTGTACATCATGCAATTTGCAAAATCTTAGTGAAGGAGAAATACGAGGCTTTGGGCGAG	613
Db	541	GTGTACATCATGCAATTTGCAAAATCTTAGTGAAGGAGAAATACGAGGCTTTGGGCGAG	600
Qy	614	GCTGGGTACCCAAATATCAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATG	673
Db	601	GCTGGGTACCCAAATATCAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATG	660
Qy	674	ATACAGTGAACACTACTCTGGTATGTAATACCACTTGGAGCAATATCATGACTCACG	733
Db	661	ATACAGTGAACACTACTCTGGTATGTAATACCACTTGGAGCAATATCATGACTCACG	720
Qy	734	GTTTATCAAGTTTATGTTCTGGACTGGTACTCTTATCTGGGAAACACAGCCGATGTCA	793
Db	721	GTTTATCAAGTTTATGTTCTGGACTGGTACTCTTATCTGGGAAACACAGCCGATGTCA	780
Qy	794	TCAAAGCAGAAATGAATCAACAGAGATAAACAGGAAGGGGACTTTTGTATAAAT	853
Db	781	TCAAAGCAGAAATGAATCAACAGAGATAAACAGGAAGGGGACTTTTGTATAAAT	840
Qy	854	CATCGACTGACTGCTTGAATTCAGGCTGTTCAAGGTGAAGATTCATGAGTCTATATAAG	913
Db	841	CATCGACTGACTGCTTGAATTCAGGCTGTTCAAGGTGAAGATTCATGAGTCTATATAAG	900
Qy	914	GCTTTTATCAATCTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	973
Db	901	GCTTTTATCAATCTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	960

Qy	974	AAAAATCAGAGATGAGTGGAGTCAGTCCATTTAA	1011
Db	961	AAAAATCAGAGATGAGTGGAGTCAGTCCATTTAA	998

Search completed: September 24, 2004, 09:23:23
Job time : 3503 secs